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January 29, 2004, 10:02:32; Search time 4104 Seconds (without alignments) 16417.679 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                               2888711 segs, 20454813386 residues
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Maximum Match 1008
Listing first 45 summaries
                                            nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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1. gb_ba:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	LIU45241 Lawsonia in W86549 Amoeba nrot	AJ43908	M31918 L	AB05741	BBGROELT Z15160 B.bacıilito	M98257	AJ24359	5 U78515 B	M91673 Le		AJ439085		AX602153	AE014285 Streptoco	AL766855	X98853 F.	AX067460	AF389514	AY256822	AJ439083	AF325222 Streptoco	D85628 Bucnnera ap	AFO08210	7 AX416527	5 AX413015	1 AL596171	7 AX417047	24	,	AKZ/4513 US CONCINGACION (6 O	AJ344978	1 AE016801	3 AF335323	9 AE015019	2 AL591982	AX641670	71 AX641671	AF387863	GROESL M91030 Ha	34719 AF434719 Buchnera
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ALIGNMENTS

RESULT 1
LIU45241
Son ribosomal binding protein homolog, GroBS/HSP10 homolog, L21
50S ribosomal binding protein homolog, GroBS/HSP10 homolog, and
GroEL/HSP60 homolog genes, complete cds.
U45241
U45241.1 GI:359919
KEXYWORDS
SOURCE
Lawsonia intracellularis
CRGANISM
Bacterria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
Desulfovibrionaces; Lawsonia.

REFERENCE
1 (bases 1 to 4710)

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2828 ACACTTGTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGT
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                                          table=11
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Best Local Similarity 100.
Matches 1647; Conservative
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                 and Strugnell, R.A. Identification and sequencing of the grob operon and flanking genes of Lawsonia intracellularis: use in phylogeny Microbiology 144 (Pt 8), 2073-2084 (1998)
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Dale, C.J., Moses, E.K., Ong, C.C., Morrow, C.J., Reed, M.B., Hasse, D.
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100.0%; Pred. No. 2.4e-283;
iive 0; Mismatches 0;
protoporphyrinogen oxidase (hemK)
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                                  2888 TTTGGTGAACGCCGTAAAGCTATGCTTGAAGATATTGCTATCCTTACTGGAGGAGAAGCA
                                                                                                              2948 ATATTTGAAGATCGTGGTATAAAGCTTGAAAATGTAAGCTTGTCTTCTTTAGGAACAGCT
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Amoeba proteus symbiotic bacterium Amoeba proteus symbiotic bacterium Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales; Legionellaceae. 1 (bases 1 to 2672) Ahn,T.I., Leeu,H.K., Kwak,I.H. and Jeon,K.W.

ORGANISM

AUTHORS TITLE

REFERENCE

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IABAMEKVGKEGVITVEDGNGIENELSVVEGNGFDRGYISPYFINNQQMKABELEHPP
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APGFGDRRKAALQDIAILINGQVISBEIGTSLETASIESSLGTPKRIVVTKENTTIIDG
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                                                                     Ann, T.T., Lim, S.T., Leeu, H.K., Lee, J.E. and Jeon, K.W. A novel strong promoter of the groEx operon of symbiotic bacteria in Amoeba proteus
Gene 148 (1), 43-49 (1994)
                                                                                                                                                                                                                                                                            Submitted (05-FEB-1992) Kwang W. Jeon, Zoology, University of Tennessee, Cunberland Street, Knoxville, TN 37996-0810 On Mar 30, 1998 this sequence version replaced gi:155400.

Location/Qualifiers
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gene isolated from symbiotic bacteria of Amoeba proteus Endocyt. Cell Res. 8, 33-44 (1991)
2 (sites)
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232_.691
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1208 CAAGAGCTGCGGTTGAAGAAGGTATTGTCCCTGGTGGTGGTACTGCTTTTGTCCGCTCCA 1267
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The evolution of the heat-shock protein GroßL from Buchnera, the primary endosymbiont of aphids, is governed by positive selection Mol. Biol. Evol. (2002) In press
2 (bases 1 to 1662)
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1562 ATCGCCGTAAAGCAATGTTGCAAGATATTGCTATCCTGACTAACGGCCAAGTGATTTCTG
                                                           AAGATCGTGGTATAAAGCTTGAAAATGTAAGCTTGTCTTCTTTAGGAACAGCTAAAACGTG
                                                                                               1622 AAGAAATTGGCACAAGCTTAGAAACCGCTTCTCTGGAAAGCTTAGGAACTGCAAAACGTA
                                                                                                                                                                    1682 TCGTTGTTACCAAAGAAACACAACCATTATCGATGGCGAAGGCAAAGCAACTGAAATCA
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Buchnera aphidicola (Tuberolachnus
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P.O. Box 2085, Valencia
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/specific_host="Tuberolachnus salignus aphid"
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/function="molecular chaperonin"
                                                                                            /organism="Buchnera aphidicola
           Direct Submission
Submitted (12-MAR-2002) Sabater-Munoz
& Biol Evol, Universidad de Valencia,
E-46071, SPAIN
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/product="GroBL protein"
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CTGCTACTGAAACTGAAATGAAAGAAGAAGGATCGTGTAGAAGATGCTCTAAATGCAA 1207
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AAGATAAGTTTGAAAATATGGGCGCTCAAATGGTTAAAGAAGTAGCTCCCAAAACTAGCG
                                                                                                                                                                                       278 ATACTGCTGGTGATGGTACTACTGCAACAGTATTGGCTCGTTCTATTCTTGTTGAAG
                                                       AGCATCGTTTCATGAACATGGCGCTCAAATGGTTAAAGAAGTGGCTTCTAAAACTTCTG
                                                                                                                                                                                                                                                  308 GIGIAAAACTIGIAGCAGCIGGICGIAAICCIAIGGCCATIAAACGIGGCAIAGAIAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        428 AAATAGCTCAAGTTGGAACCATTTCTGCAAACTCTGATACAACAATAGGTAATATCATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             518 CTGAAGCAATGCAAAAGTTGGTAAAGAGGGTGTTATTACCGTTGAAGATGGTAATGGAT
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                                                                                                                  1811 bp DNA linear BCT 26-APR-1993 pneumonphila htp heat shock operon HtpB (hptB gene),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APTVTKDGVSVAKEI EFEHRFMNMGAQMVKEVASKTSDTAĞDGTTTATVLARSILVEG
HKAVAAGMNPMDLKRGIDKAVLAVTKKLQAMSKPCKDSKAIAQVGTISANSDEAIGAI
IAEAMEKVGKEGVITVEDGNGLENELYVVEGMQPDRGYISPYFINNQQNMSCELEHPF
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AFGFGRRKAALQDIALITKGQVISEBEIGKSLEGATLEDLGSAKRIVYTKENTTIIO
EGKATEIINAEIAQIETAZQMEETTSDVDREKLOGRVAKLAGGVAVIKVGAATEVENKEKK
ARVEDALHATRAAVEEGIVAGGGVALIRAQKALDSLKGDNDDQNRGINILRRAHESPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'translation="MAKELRFGDDARLQMLAGVNALADAVQVTMGPRGRNVVLEKSYG
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VASLMLTTECMVADLPKKEEGVGAGDMGGMGGMGGMGMM"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Original source text: Legionella pneumophila (strain SVir) (library: cosmid clone pHC79) DNA.

Taft entry and computer-readable sequence for [Unpublished (1990) Univ. of TN at Memphis, Memphis TN 38163] kindly submitted by P.S. Hoffman, 05-FBB-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITATGGCGCTCCTACTGTAACTAAAGACGGTGTGTCTGTTGCCAAAGAATTGAATTTG 217
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                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                   Legionellaceae; Legionella.

(Dases 1 to 1811)

Hoffman, P. S., Houston, L. and Butler, C.A.

Legionella pneumophila htpAB heat shock operon: nu and expression of the 60-kilodalton antigen in L. pneumophila-infected Heba cells

Infect Immun. 58 (10), 3380-3387 (1990)
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Pred. No. 1.1e-128;
0; Mismatches 521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:446"
/tissue_lib="cosmid_clone_pHC79"
34. 1680
/gene="htpB"
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/db_xref="GI:149692"
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/strain="SVir"
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/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                      htp heat shock operon.
Legionella pneumophila
Legionella pneumophila
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Best Local Similarity 67.7%;
Matches 1107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-FEB-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1291 ATCATTGCAGAAGCAATGGAAAAAGTAGGCCGTAATACAGGTGTTATTACTGTTGAAGAA 1350
                                 /trānslation="MNIRPLQDRVIVKRLEEETKSAGGIVLTGSAAEKSTRGEVVAVG
NGRILDNGDVRALEVKAGDTVLFGSYVEKTEKIEGQEYLIMREDNILGIVG"
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Pred. No. 1.8e-128;
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xref="GI:13366172"
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    CTATTGTTGTAGAAAAGTTCGTGAACCAAAAGATGGTTTTGGATTTAATGCTGCATCAG 1447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete cds.
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Alteromonadaceae; Pseudoalteromonas.
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                                                                                                                                                                                                                                                                                                                                                                      1418 chgrichacharchagchagchchacharchachachachachachacha
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/strain="PS1M3"
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1. .2715
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Pseudoalteromonas sp. PS1M3
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/trans1_table=11
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Moleculer chaperone of Ps
Unpublished
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458. .464
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474. .761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1652 GAATGGGTGGCATG 1665
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MIADAMEKVGNEGVITVEEAKTAETELEVVEGMOFDRGYLSPYRVINSERMOLDDD
YILHEKKLSNLQSLLPVLEAVAQSGKPLLITAEDVEGALATLVNKLRGGLKIAAV
KAPGFGDRRKAMLEDIAVLTGGQVISEDVGIKLBUVTLEMLGRAKKVINSKETTITVD
GAGGKESINNEVOQIKAQIEETTSDYDREKLQBRLAKLAGGVAVIRVGGSTEVKEK
KDRVDDALNATRAAVEEGIVPGGGTPLLRARAAGGVAVIRVGGSTEVKEK
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GVKAVAASMNPMDLKRGIDAAVEAVVADLFKKAKKIQTSEEIAQVATISANGAEDIGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RQIAHNAGEEAAVIVGKVLENCSDTFGYNTATAQFRDLISFGIVDPVKVVRSALQNAA
SIASLLITTEAMVAEVPKKEAAAPAMPGGGMGGMDF"
283 c 425 g 456 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MAAKEVKFGRDARERLLRGVDILADAVKVTLGPKGRNVVIDKSF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GAAAAGTCTTTTGGTTCCCCAGTTATTACAAAAGATGGTGTATCTGTTGCAAAAGAAATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATAAATCATTTGGTGCTCCACGCATTACAAAGATGGTGTGTGCGTTGCAAAAGAAATC 180
                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (25-SEP-1992) Michael G. Schreiber Dr., Virologie,
Bernhard Nocht Institute for, Tropical Medicine,
Bernhard-Nocht-Strasse 74, Hamburg, Hamburg, D-2000 Hamburg 36,
                                         B.bacilliformis GroEL-type gene encoding heat shock protein 60. 215160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATATCCTTGCTGATGCTGAGGTAACACTTGGTCCTAAAGGCCGCAATGTGGTGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGGCTGCTAAAAAGTAAAATTTTGGCCGTGACGCACGTGAAAGGTTGTTACGTGGTGTG
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                                                                                                                                                                                Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales,
                                                                                                                                                                                                                                                            The 60 kD heat shock protein of Bartonella bacilliformis
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                                                                                                                      groEL gene; heat shock protein; heat shock protein 60.
Bartonella bacilliformis
Bartonella bacilliformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:774"
/chromosome="5 kb EcoRI genomic DNA fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="Bartonella bacilliformis B13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HSP 60)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Bartonella bacilliformis"
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Pred. No. 2.1e-127;
); Mismatches 508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="heat shock protein 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAA78859.1"
/db_xref="G1:397596"
/db_xref="SWISS-PROT:P35635"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard_name="Bb HSP
                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                Bartonellaceae, Bartonella.
1 (bases 1 to 1635)
Schreiber, M.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="GroEL-type"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="GroEL-type"
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'trans1 table=11
'product="GroBL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="7B2"
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68.3%;
                                                                                                                                                                                                                                                                                                 2 (bases 1 to 1635)
Schreiber, M.G.
                                                                                                  Z15160.1 GI:397595
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BBGROELT
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                                                                                                                                                                                                                                                                                                                                                                                                                                GTTAITICTGAAGAAATIGGCCTTGAGCTTGAAAAGCAACAGTTGAAGACCTAGGTACA 1770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGATATTAAAAGTCCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAAGCTCAGAT 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2371 ATGGTTGCTGAAATCCCTAAAGAAGAAGCTGCTGGTGCCCCTGATATGGGTGGCATGGGC 2430
                                  CTATCTCCTTACTTAACAACGCTGAAAAGGCGCAGTTGAATTAGATAACCCATTT
                                                                                                            1471 ATTCTACTIGTAGATAAAAAGTATCTAACATTCGTGAGCTACTACTACATTAGAAGCC
                                                                         ATCCTTTGTAATGAGAAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAA
                                                                                                                                                                                                                                                                                                             GGTTTTGGTGAACGCCGTAAAGCTATGCTTGAAGATATTGCTATCCTTACTGGAGGAGAA
CTCTCTCCATACTTTGTAACTAATCCTGAGAAAATGGTTTGTGAACTTGATAACCCTTAT
                                                                                                                                                     GTTGCTAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTT
                                                                                                                                                                                          1531 GTTGCTAAAGCAAGCAAGCCACTATTAATCATTGCTGAAGACCTTGAAGGCGAAGCACTT
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SEAKTATELELEVVEGMQFDRGYLSPYFVTNSEKMYDLDDP
TLEAVVQSGKPLLIADEVBCERALATLVVNKLRGGIKIAAV
ILTSGQVISEDVGIKLENVTLEMLGRAKKVHVSKETTTIVD
DIETTSDYDREKLÜGRLAKLAGGVAVIRVGGSTBYBVKEK
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Haake, D.A., Summers, T.A. and Schwartzman, W.
Direct Submission
Submitted (15-NOV-1996) Medicine, 111F, West Los Angeles VAMC,
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GAPRITKDGVSVAKEIELBDKFENMGAQMLREVASKTNDIAGDGTTTATVLGQAIVQB
GYRAVBAGMNEPMILKRGFIDAAVDEVVANALFKKRKKTGYSAEIAQVGTISANGABIGK
MIADAMEKKYGNEGVITYEBATVETELEVVBAVLEKKKRKTGYSAEIAQVGTISANGABIGK
MIADAMEKKANGGVILPVEBATVAGSGKFLLIITABDVEGRALATLIVVNKLRGGIKIAAV
KAPGFGDRRKAMLEDIAILTSGQVISEDVGIKLENVTLDMLGRAKKVNISKENTTIID
GAĞÇKSEINARNYQIKVQIEBTTSDYDERKLQERLAKLAĞGAVIRVGGATEVEVKEK
KONUDALNATRABUNGIKVQIEBTTSDYDERKLQERLAKLAĞGAVIRVGGATEVEVKEK
KONUDALNATRABUNGIKVQIEBTTSDYDERKLGERLAKLAĞGAVIRVGGATEVEVKEK
KORVDDALNATRABUNGEGILVAGGTALLRAANALTVKGSNPDQEAGTNIVRRALQABA
SIASILITTEAMVAEVEKOTFVPPPMEGGGMGGMGGMGGMGFN"
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USA
90073,
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transl_table=11
product="heat shock protein HSP60"
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Pred. No. 2.7e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 2.7e-127;
0; Mismatches 514;
                                                                             /organism="Bartonella henselae"
/mol_type="genomic DNA"
/strain="ATCC 49882"
/d_xref="taxon:38323"
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  Angeles,
                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAB69094.1"
/db_xref="GI:2358234"
              Location/Qualifiers
1. 1644
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  Wilshire Blvd., Los
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note="GroEL"
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Best Local Similarity 68.1
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GSPVITKDGVSVAKEIELEDKFENMGAOMVKEVASKANDAAGDGTTTATVLAQSIVNE
GLKAVAAGMNPMDLKRGIDKAVIAAVAELKALSVPCSDTKAIAQVGTISANSDKEIGD
IIAQAMEKVGRNSGVITVEEGQSLENELDVVEGMQFDRGYLSPYFINSPEKGTVELDN
                                                                                                                                                                                                       PFILLVDKKI SNIRELLPTLEAVAKASKPLLI IAEDLEGEALATLVVNNMRGI VKVSA
VKAPGFGDRRKAMLQDIAVLTGGTVI SEEIGLELEKATVEDLGTAERVI ITKDDTTI I
DGAGEEAGINGRVSQI KAQI EEATSDYDKEKLQERMAKLAGGVAVI KYGAATEMEMKE
                                                                                                                                                                                                                                                                           KKDRVEDALMATRAAVEEGVVPGGGVALVRAASKLVDLVGDNEDQNHGIKVALRAMEA
PLRQIVTNAGDEASVVINAVKAGSGNFGYNAATGEYNDMIEMGILDPTKVTRSALQFA
                                                                                                                          translation="MAAKEVLFAGDARAKMLTGVNILANAVKVTLGPKGRNVVLDKSF/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  984 ATCATTGCACAAGCAATGGAAAAAGTAGGCCGTAACAGTGGTGTTATTACTGTAGAAGAA 11043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1044 GGTCAATCACTAGAAATGAACTCGATGTTGAAGGCATGCAGTTTGACCGTGGTTAC 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATAAACTIGCAAAIGCIGTIAAAGIAACACTIGGACCIAAAGGCCGIAAIGICGTIATI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAAAGTCTTTTGGTTCCCCAGTTATTACAAAAGATGGTGTATCTGTTGCAAAAGAAATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  624 GATAAATCATTTGGCTCTCCAGTTATCACTAAAGATGGTGTATCTGTAGCAAAAGAAATC 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAACTTGAAGACAAGTTTGAGAACATGGGCGCACAAATGGTTAAAGAAGTTGCATCTAAA 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 ACTAGCGATATTGCTGGTGATGGAACTACAACAGCAACAGTCCTTGCACAAGCTATTTAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    744 GCTAACGAIGCAGCCGGCGAIGGTACAACTACCGCTACAGTACTIGCACAGICTATIGIA 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTGAAGGTGTAAAACTTGTAGCAGCTGGTCGTAATCCTATGGCCATTAAACGTGGCATA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACGAAGGCCTTAAAGCTGTTGCAGCATGAACCCCAATGGACCTTAAGCGCGGCATC 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATAAAGCTGTTGTTGCTGTTACTAAAGAACTAAGCGACATTACAAAGCCTACTCGTGAC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 CAAAAAGAAATAGCTCAAGTTGGAACCATTTCTGCAAACTCTGATACAACAATAGGTAAT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          924 actaaaccaatrecacaagractactartreactaacteaaraaagaarregeeae 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       658 ATCCTTTGTAATGAGAAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAA 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             504 Arddcagcaaaadaadracririrircaggraacgcacgcaaaagcraaargcraacraacgcara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 564 AACATCCTGGCAAACGCAGTAAAAGTTACATTAGGTCCTAAAGGCCGTAACGTTGTACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAACTTGAAGATAAGTTTGAAAATATGGGCGCTCCAAATGGTTAAAAGAAGTAGCTCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGGCTTCTAAAGAAATCCTTTTTGATGCTAAAGCCCGTGAAAAACTTTCACGAGGTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         864 GACAAAGCAGTAATTGCTGCTGCTGCAGAGCTTAAAAGCGTTATCTGTTCCATGCTCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCATAGCTGAAGCTATGGCTAAAGTTG---GAAAAGGAGGTGTTATCACAGTTGAGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.4%; Score 764.6; DB 1; Length 2241; 67.4%; Pred. No. 3e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                GSIAGLMITTEAMVAEIPKDDSAPDMGGMGGMGGMGGMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 529;
                 /trans1_table=11
/product="GroEL_protein"
/protein_id="CAB50775.1"
/db_xref="G1:5524758"
/db_xref="SPTREMBL:Q9XAU7"
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                                                                                                                                                                                                                                                                                                                                                                                                                       511
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Direct Submission
Submitted (12-JUL-1999) Tosco A., Organic and Biological Chemistry, University of Naples, via Mezzocannone 16 (NA), I-80134, ITALY
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Submitted (05-FEB-2001) Stefania M., Organic and Biological
Chemistry, University of Naples, via Mezzocannone 16 (NA), I-80134,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MNIRPLHDRVIVKRLEEETKSAGGIVLTGSAAEKSTRGEVVAVG
NGRILESGDVRALEVKAGDTVLFGSSYVEKVEKIEGQEYLIMREDNILGIVG"
                                                                                                                                   groEL gene; GroEL protein; groES gene; GROES protein.
Pseudoalteromonas haloplanktis
Pseudoalteromonas haloplanktis
Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Pseudoalteromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Feb 6, 2001 this sequence version replaced gi:5524757 Location/Qualifiers
                                                                                                                                                                                                                                                                Tosco, A., Birolo, L., Scaloni, A., Sannia, G. and Marino, G. A GroEL-like protein from the psychrotrophic bacterium Pseudoalteromonas haloplanktis TAC125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'organism="Pseudoalteromonas haloplanktis"
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evidence=experimental
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function="molecular co-chaperone"
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RQU78515 16-SEP-1997 2017 16-SEP-1997 Bartonella quintana heat shock protein HSP60 (groEL) gene, complete

U78515

ACCESSION

cds.

RESULT 10 RQU78515 LOCUS DEFINITION

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YILIHEKKLSNIÇSILPVLEAVVOSGKPLLIIAEDVEGEALATLVVNKLRGGIKTAAV
KARGEGDRRKAMLEDIAILTSGQVISEDVGIKLENVTLDMLGRAKKVNISKENTTIID
GAGKKAEINARVNQIKVQIEETTSDYDREKLQERLAKLAGGVAVIRVGATEVBVKKK
KDRYDDAINATRAAVEEGIYAGGGTALLRAANALAIKGSNPDQEAGINIVRRALQAPA
RQIATNAGEEAAIIVGKVLENNADTFGYNTATGGFGDLIALGIVDPVKVVRSALQNAA
SIASLLITTEAMYARVPKKDTPMPPRGGGMGGMDF"

298 c 433 g 435 t
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GVKAVAAGMNPMDLKRGIDAAVEEVVGNLFKKAKKIQTSAEIAQVGTISANGAAEIGK
MIADAMEKVGNEGVITVEEAKTAETELEVVEGMQFDRGYLSPYFVTNADKMVADLDDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="heat shock protein HSP60"
|protein id="AAB69051."
|db_xref="G1:2358236"
|txanslation="WAAKEVKFGREARERLLRGVDILANAVKVTLGPKGRNVVIDKSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GATAAATCGTTTGGTGCGCCTCGCATCACAAAGATGGTGTATCTGTTGCAAAAGAATC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 ACTAGCGATATTGCTGGTGATGGAACTACAACAGCAACAGTCCTTGCACAAGCTATTTAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 ACCAATGACATTGCTGGGGATGGAACAACAACTGCTTTTAGGACAGGCTATTGTA 300
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                                                                                                                                         Haake,D.A., Summers,T.A., McCoy,A.M. and Schwartzman,W. Heat shock response and groEL sequence of Bartonella henselae Bartonella quintana
                                                                                                                                                                                                                                                                                                                                     Los Angeles VAMC,
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                             Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bartonellaceae; Bartonella.
1 (bases 1 to 1644)
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                                                                                                                                                                                                                                                                                                                                     Submitted (15-NOV-1996) Medicine, 111F, West 11301 Wilshire Blvd., Los Angeles, CA 90073, Location/Qualifiers
                                                                                                                                                                                                                                                                                               Haake, D.A., Summers, T.A. and Schwartzman, W. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 762.6; DB 1;
Pred. No. 7.1e-126;
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                                                                                                                                                                                                         Microbiology 143 (Pt 8), 2807-2815 (1997) 97419519
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Bartonella quintana"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="ATCC 51694"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:803"
1. .1644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              table=11
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/transl_table=
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Best Local Similarity 67.8%;
Matches 1113; Conservative
  GI:2358235
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                                            Bartonella quintana
                                                                Bartonella quintana
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1558 GCTATTGCTGAAAAACCAGAACCTAAAAAAGATATGCCT---ATGCCTGGCGGTGGTATG 1614
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HKAVAAGMNPMDLKRGIDKAVLAVTKKLQAMSKPCKDSKAIAQVGTISANSDEAIGAI
IAEAMEKVGKEGVITVEDGNGLENELSVVEGMQLIAVHSPYFINNQQNMSCELEHPFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGFGDRRKAMLQDIALLTKGQVISEEIGKSLEGATLEDLGSAKRIVVTKENTTTIDGE
GKATEINAR TQIRAQMEETTSDYDREKLQERVAKLAGGVAVIKVGAATEVENKEKKA
RVEDALHATRAAVEEGIVAGGSVALIRAQKALDSIKGONDDQNMGINILRRALESPMR
QIVTNAGYERSVVNKVAEHKDNYGENAATGEYGDWYERMGILDPTKVTRMALQNAASV
ASLMLTTECNVADLPKKEEGVGAGDMGGMGGMGGMGGMG
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'db_xref="GI:149690"
'translation="MAKBLRFGDDARLQMLAGVNALADAVQVTWGPRGRNVVLEKSYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LL/UDKKVSSIREMLSVLEGVAKSGRPLLIIAEDVEGEALATLVVNNMRGIVKVCAVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene, complete
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                                                                                                                                                        1498 GIGCGIICIGCICICCAGAAIGCIGCAICGAITGCCAGCCIICTCAICACAACAGCA
                                                                                                                                                                                                                                 1558 ATGGTTGCTGAAGTTCCAAAGAAAGAAGACACTCCAATGCCTCCAATGCCTGGTGGCGGAATG
                                                                    1438 ACCGCAACTGGTCAATTTGGTGATTTGATTGCTTTAGGAATCGTTGATCGTGGGTT
                                                                                                               1498 ACACGTATTGCATTACAAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGC
                           1438 GCTGCATCAGGAGAATATGAAGACCTTATTAAAGCTGGTGTCATTGATCCTAAAAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gammaproteobacteria; Legionellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumophila gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Legionellal Legionellalaceae; Legionella.

[Logaes 1 to 2016]
Sampson, J.S., O'Connor, S.P., Holloway, B.P., Plikaytis, B.B. Carlone, G.M. and Mayer, L.W.

Nucleotide sequence of htpB,
encoding the 58-kilodalton (kDa) common antigen, formerly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
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Pred. No. 1e-124;
); Mismatches 525; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          LPNHTPB 2016 bp DNA linear Legionella pneumophila 58-kDa common antigen (htpb)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Legionella pneumophila"
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|transl_table=11
|product="58-kDa common antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    designated the 60-kPa common antigen
Infect. Immun. 58 (9), 3154-3157 (1990)
90354095
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/strain="Philadelphia 1"
/sub_species="pneumophila"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M91673.1 GI:149689
58-kDa common antigen; htpB gene.
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Location/Qualifiers
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211. .1854
                                                                                                                                                                                                                                                                                        GGTGGTATGGGTGGTATGGAC 1635
                                                                                                                                                                                                                                                                                                                                 1618 GGTGGAATGGGCGGAATGGAC 1638
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/gene="htpB"
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Best Local Similarity 67.3%;
Matches 1100; Conservative
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTAT 1080
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                                                                                    361 GATGCTGCTGTTGAAGAAGTGGTGGTGATCTTTTCAAAAAAAGCGAAAAAATCCAGACT
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8 CTAAAGAATCCTTTTTGATGCTAAAGCCCGTGAAAAACTTTCACGAGGTGTAGATAAAC 67 215 CTAAAGAATTACGTTTTTGATGATGACGCTCGCCTTACAAATGCTTGCT	188 AAGATAAGTTTGAAAATATGGGCGCTCAAATGGTTAAAGAAGTAGCTCCCAAAACTAGGG 247 395 AGCATCGTTTCATGAACATGGCGCTCCAAATGGTTAAAGAAGTGGCTTCTAAAACTTCTG 454 248 ATATTGCTCGTGATGGAACTACAACAGCAACAGTCCTTGCAAAGCTATTATCGTGAAG 307	515 GTCACAAAGCAGTTGCTGCTGCTAATGATCCAAAGGCGCTGTTGATTGA		992 TÄĞTCÄÄCAÄCATGCĞGTATTGTAAÄĞTATGTĞCTĞTCÄÄĞĞĞĞCTĞĞTTTTĞĞTĞ 1051 848 AACGCCGTAAAĞCTATGCTTGAAĞATATTGCTACTGGAGGAGAAĞGCATATTTG 907 1052 ATCGCCGCAAAĞCGATGTTGCAAĞACTTGCTATTTGACTAAGGGTCAAĞTTATTTG 1111 908 AAGATCGTGGTATAAAGCTTGAAAATGTAAĞCTGTTGTTTTTGGAACGTCAAĞTTATTTCTG 1111 1112 AAGAAATTGGCAAĞACTTGAAAATGTAAĞGTTGTTGTTGTAĞTAĞTTATTTTG 1111 968 TAGTTATTGACAAAGAAAATACTACTATCGTTGGTGCTGGAAAATCAGAAGATTA 1027 1172 TCGTTGTTACCAAAGAAAATACTGCTCATTGATGGTGCTGGAAATCAGAAATTA 1231 1173 AAGTGGTGGTTAAAAAATGAAGAAATGAAGGAAAGGGAAAGGCAAATTA 1231 1174 AAGTTAACTAAAAATTCATGGCACAAATGAAGAAAAGGGCAACTGAAATTA 1231 1175 AAGTCGGTTAAAAAATACTGCCACAAATGAAGAAAAAGGGCAACTGAAATTA 1231 1176 AAGTCGGTTAAAAAAATACTGCCACAAATGAAGAAAAAAAGGGAAAAGGCAAATAAGAAATGAAGAAAAAAAA
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                                                                                                                                                                                                                                                                                    CAAAACTTGTTGGTGGAGTAGCTGTTATCCATGTTGGAG 1147
                        CTAAACTAGCTGGTGGTGCTGTTATCAAGTTGGCG 1351
                                                                                                           AAGAGAAGAAAGCACGTGTTGAAGATGCTCTTCATGCTA 1411
                                                                                                                                                                                                                                                                                                                                       CTTTACGTCAAATTGCTGCAAATGCTGGCTATGAAGGTT 1387
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                                                                                               ACGCTCGTTGTCAACAAACTGCGTGGTGGTTTGAAAATTGCTGCTGTGAAAGCTCCAGGA
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Buchnera aphidicola (Thelaxes suberi)
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/db_xref="GI:3603159"
                                                                        /transl_table=11
/product="60 kDa heat
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GATAAAGCTGTTATTGCAGCAGTAGAAGAACTTAAATGTCTTTCTGTTCCTTGTTCTGAT 420
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                                             CAAAAAGAAATAGCTCAAGTTGGAACCATTTCTGCAAACTCTGATACAACAACAATAGGTAAT
                                                                                                                                                                                TTAATTGCAGAAGCAATGGAAAAGCTTGGAAAAGAAGGTGTAATCACTGTTGAAGAAGGA
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                                                                       Fares, M.A., Barrio, E., Sabater-Munoz, B. and Moya, A. The evolution of the heat-shock protein GroEL from Buchnera, the primary endosymbiont of aphids, is governed by positive selection Mol. Biol. (2002) In press
       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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P.O. Box 2085,
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                                                                                                                                                                                                                                                                                                                                                    (Thelaxes
                                                                                                                                                                                                                                                                                                                                                  /organism="Buchnera aphidicola (Thelax,
/mol_type="genomic DNA"
/specific_host="Thelaxes suberi aphid"
/db_xref="caxon:88797"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="groEL"
'function="molecular chaperonin"
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E-46071, SPAIN
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OY 1501 CGTATTGCATTACAAATGCACATCACTAGCTTCTTACTTCTACTACAAATGCCT 1560	Query Match Best Local Similarity 67.6%; Score 751.2; DB 1; Length 2770; Best Local Similarity 67.6%; Pred. No. 7e-124; Matches 1104; Conservative 0; Mismatches 519; Indels 12; Gaps 3; Oy 87. CTARAGARATCTGTTTGATGCTARAGCCGGTARAAGCTTGCGGGTGTAACGCAT 531 Oy 68 TIGCAATGCTGTTTGGGGACGATGCTCGTCAACGACGTGTAACGCAT 531 OY 128 TIGCAATGCTGTTAAGCTAACGCGTCAACGACGTAATGCTTGTTTGAAAGAT 127 Db 532 TGGCTGATGCACTTTTGAACGATGATGCTTAACGAACGTTATTTGAAAGAT 591 OY 128 CTTTTGGTTCCCCAATGACAATGGGTCTTTTTGTAACATT 591 OY 128 AAATAACTTTGAAAATATGGCGCTCAAATGGTTTAAAGAAATTGAATTCG 651 OY 128 AAATAACTTTGAAAATATGGCGCTCAAATGGTTTAAAGAAATTGAATTCG 651 OY 128 AAATAACTTTGAAAATATGGCGCTCAAATGGTTTAAAGAAATTGAATTCG 651 OY 188 AAGATAAGTTTGAAAATATGGCGCTCAAATGGTTTAAAGAAATTGAATTCG 651 OY 248 AAATAGCTTGAAAATATGGCGCTCAAATGGTTTAAAGAAATTGAAACTTCTG 711 OY 248 AAATAGCTTGAAAATATGCGCCCCAAAATGGTTAAAGAAGTAGCTCTGAAAGTTTAATGAAAG 307 III III III III III III III III III I

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                                                                                           A DNA molecule (AAT69201) codes for the GroEL heat shock protein (AAM16678) of Lawsonia intracellularis, the causative agent of porcine proliferative enteropathy (PPE). A genomic library was prepd. from L. intracellularis PPE lesion isolates and screened with rabbit anti-L. intracellularis antiserum. Phagemid DNA was isolated from individual clones and sequenced. GroEL and GroES (see also AAT69202)
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                                                                                                                                                                    individual clones and sequenced. GroEL and GroES (see also AAT69202 sequences were identified and another 13 clones were subsequently (AAT69203-15) isolated. These nucleic acids can be used to produce recombinant polypeptides useful in vaccines against intestinal diseases such as PPE, including recombinant vaccines utilising bacterial, fungal or viral vectors. They can also be used as genetic vaccines and in diagnostic assays.
             Vaccine for treating or preventing Lawsonia intracellularis infection - especially in pigs, containing non-pathogenic form of bacterium or its components
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                                                                                                                                                                                                                                                                                                                   DNA molecules (AAT69203-15) were isolated from an immunoscreening of a Lawsonia intracellularis library using experimental sera from vaccinated pigs. These nucleic acids, as well as isolated GroEL and GroES (AAT69201-02) sequences, encode putative vaccine candidates (see also AAW16678-85) useful for protection of animals and birds against intestinal diseases, esp. protection of pigs against porcine proliferative enteropathy (PPE). They can also be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2048 AIGGCIICIAAAGAAICCIIIIIGAIGCIAAAGCCCGIGAAAAACIIICACGAGGIGIA
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                            Intestinal disease; porcine proliferative enteropathy; vaccine;
                                                                                                                                                                                                                                                   Vaccine for treating or preventing Lawsonia intracellularis infection - especially in pigs, containing non-pathogenic form bacterium or its components
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        Lawsonia intracellularis vaccine candidate DNA
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100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                Claim 14; Page 47-50; 94pp; English.
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PIG RES & DEV CORP.
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                                                    Lawsonia intracellularis
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Matches 1647; Conserv
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                                                                                                    481 ATCATAGCTGAAGCTATGGCTAAAGTTGGAAAAGGAGGTGT
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68.0%;

Best Local Similarity

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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus progenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71256 and antibaches that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in a biological sample. (I) are used to detect Streptococcus in a biological sample. (I) are used to detect Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity concerns the concerns of the composition (I) are used for affinity concerns the concerns of the composition of 
3548 CGTATTGCATTACAAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGCGCT 3607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                 ATTIGCTGAAAAACCAGAACCTAAAAAAATATTGCCTATGCCTGGCGGTGGTATGGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus polynucleotide SEQ ID NO 6231.
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                                                                                                                                                                                 3668 AIGGGIGGTAIGGACGGIAIGIACTAG 3694
                                                                                                                                                      ATGGGTGGTATGGACGGTATGTACTAG 1647
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                                                                                                                                                                                                                                                                                                                                        ABN69159 standard; DNA; 1620
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(GENO-) INST GENOMIC RES
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Tettelin H;
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                                                                                   AAAAATTACAAGAACGACTTGCTAAGTTAGCCGGTGGTGGTAGCAGTAATTAAAGTTGGTG
                                                                                                                             CTGCTACTGAAACTGAAATGAAAGAAGAAGAATCGTGTAGAAGATGCTCTAAATGCAA
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streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiminfammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antiboddes that bind (I) are used in the manufacture of medicaments for antiboddes that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to recombinantly produce (I), may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chroming produce (I) and may be chromatography, immunoassays, and distinguishing/identifying
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New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2024145 CATTTGGTTCTCCTTTAATTACAATGATGGTGTGACAATTGCTAAAGAAATTGAGCTAG
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                                                                                                                                                        relates to a protein (ABP25413-ABP30895) from group B
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Pred. No. 2.6e-161;
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                                                                                                           Claim 8; Page 4196-4488; 4525pp; English.
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                                                              TAAACCGTCCACTCCTTATTATTGCTGAAGGTGAAGGTGAAGCACTTGCAACATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAP28514-AAP28554). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as ottics media, sinustits and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          427
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                                                             otitis media; sinusitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 96109;
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Pred. No. 1.3e-160;
); Mismatches 547;
                                                          human upper airway;
                                                                                     endocarditis; meningitis; ss
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66.3%;
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                                                        Genomic library; bacteria;
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Matches 1086; Conservative
                                                                                                                                          Moraxella catarrhalis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patterson
Genomic fragment #35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-041427/05.
                                                                                     bronchopulmonary;
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1508 CATTACAAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGCGCTATTGCTG 1567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication
                                                                                                        CTAAAGAAATCCTTTTTGATGCTAAAAGCCCGTGAAAAAACTTTCACGAGGTGTAGATAAAC
                                                                                 1568 AAAAACCAGAACCTAAAAAAGATATGCCTATGCCTGGCGGTGGTATGGGTGGTATGGGTG
                                       50780 CATTAGAACATGCTGCTTCTGTCGCAGGTTTGATGTTGACCACTGAGGTGATTACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibacterial; Listeria; food contamination; mutational analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and pathogenicity of Listeria (potential therapeutic agents), ālı
treating infections by Listeria, and are useful as immunogens in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the printed specification, but was obtained in electronic for directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-Listeria vaccines.
Note: The sequence data for this patent did not form part
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                                                                                                                                                                                                                                                                                                                                                                                                                            Listeria monocytogenes 4b contig DNA sequence #647
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                                                                                                                                                                 1628 GTATGGACGGTATGTACTA 1646
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Matches 1081; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Listeria monocytogenes
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                                                        49700 CGATTGCTCAAGTTGGCTCAATTTCAGCAAACTCAGATGCTACCATTGGTGAGCTTATCT 49759
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and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-listeria vaccines.
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                                                                                                                                                                                             Sequence 213251 BP; 70939 A; 36026 C; 43257 G; 63029 T; 0 other;
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BP. Listeria innocua DNA sequence #684. standard; DNA; 3011208

Antibacterial, Listeria, food contamination, mutational analysis,

WO200228891-A2

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                                                                                                                                                                                                                                                                                        (ABQ67188-ABO71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-Listeria vaccines.
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                                                                                                                                                                                                                                                                               to nucleic acid sequences
                                                                                                                                                                                             New genomic sequences from Listeria species, useful
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2195857 CAGAAGCAATGGAACGTGTTGGTAACGATGGTGTTATTACTATTGAAGAATCCAAAGGCT
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                                                                                           TTGAAACTACATTAGATGTGGTTGAAGGAATGAAGTTTGACCGTGGCTACCTCTCTCCAT
                                                                                                                                                                                   2195797 TTGCAACAGAATTAGACGTAGTAGAAGGTATGCAATTTGACCGTGGCTACACTAGTCCTT
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                                                                                                                                                                                                                                                                               ACTITICTAACTAATCCTGAGAAAATGGTTTGTGAACTTGATAACCCTTATATCCTTTGTA
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Sequence 2944528 BP; 914202 A; 563301 C; 555061 G; 911964 T; 0 other;
                                                                                            Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease; ds.
                                                                                  Listeria monocytogenes EGD-e genome sequence.
                                             ABA03041 standard; DNA; 2944528 BP
                                                                                                                                                        11-APR-2001; 2001WO-FR01118.
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                                                                                                                   Listeria monocytogenes.
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1628
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Dehoux P; Cossart P; Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart F Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann B, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J; Claim 1; SEQ ID No 1; 192pp; French.

The present sequence is the genome sequence of Listeria monocytogenes BGD-e. This sequence and fragments of this sequence are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and to study genetic polymorphisms and other genomes. Proteins (ABB47297-ABBS0149) expressed from the present sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. This sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, this sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences.

2; DB 24; Length 2944528; 43.9%; Score 722.6; DB 24; Length 66.2%; Pred. No. 9.9e-156; tive 0; Mismatches 544; Indels Conservative Best Local Similarity Matches 1075; Conserv Query Match

2148471 ATCGTGGTAAAGCAATGCTAGAAGATATTGCTATTTTAACAGGCGGACAAGTCATTACAG 2148412 2148831 CAGAAGCAATGGAACGCGTTGGTAACGACGGCGTTATCACTATTGAAGAATCCAAAGGTT 2148772 2148771 TIGCAACAGAATIAGACGIAGIAGAAGGIAIGCAATICGACCGCGGCIACACIAGCCCTI 2148712 2148711 ACATGGTAACTGATTCCGATAAATGGAAGCTGTTCTTGAAAACCATACATTTTAATTA 2148652 2148651 CAGACAAAAAATCAACAATATTCAAGAAATCTTACCAGTTTTAGAACAAGTCGTTCAAC 2148592 2148411 AAGACCTAGGATTAGAACTAAAACAGCTACTGTTGATCAACTTGGAACAGCTAACAAAG 2148352 2148351 TAGTICGTAACAAAAGATGATACAACAATCGTAGAAGGAGGAGGCGGTTICCACACAAATTA 2148292 2148291 GCGCTCGCCTAAACCAAATCCGTGCGCAAATGGAAGAACTACTTCTGAATTTGATAGAG 2148232 2149008 GCTTAAAAAATGTAACAGCTGGAGCAAACCCAGTAGGCGTTCGCCGCGGTATCGAAAAAG 2148949 2148948 CCGTAGCAACAGCTATCGAAGAATTAAAAGCTATTTCTAAACCAATTGAAAGCAAAGGAGT 2148889 2148888 CTATCGCTCAAGTTGCTGCTATTTCTTC---TGGTGATGAAGAAGTTGGTAATTAATCG 2148832 2149308 CAAAAGATATTAAAATTTAGTGAAGATGCTCGTCGTGCCATGTTAACGTGGTCGACCAAC 2149249 2149188 AATTCGGTTCTCCGTTAATTACAAATGATGGGGTAACAATTGCAAAAGAAATTGAATTAG 2149129 2149248 TAĞCAAACĞCAĞTAAAAĞTAACĞCTTĞGCCCAAAAĞGTCĞTAATGTTGTTTTAGAGAAĞA 2149189 1088 AAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGCAGGTAGCTGTTATCCATGTTGGAG 1147 1028 AAGCICGAGITAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTATGATCGTG 1087 TAGTTATTGACAAAGAAAATACTACTATCGTTGATGGTGCTGGAAAATCAGAAGATATTA 1027 847 607 ATGAGAAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTTGCTAAAG 727 907 188 AAGATAAGTTTGAAAATATGGGCGCTCAAATGGTTAAAGAAGTAGCTCCCAAAACTAGCG 247 248 ATATTGCTGGTGATGGAACTACAACAGCAACAGTCCTTGCACAAGCTATTTATCGTGAAG 307 128 CTTTTGGTTCCCCAGTTATTACAAAAGATGGTGTATCTGTTGCAAAAGAAATTGAACTTG 187 308 GIGIAAAACTIGIAGCAGCIGGICGIAAICCIAIGGCCAIIAAACGIGGCAIAGAAG 367 CTGTTGTTGCTGTTACTAAAGAACTAAGCGACATTACAAAGCCTACTCGTGACCAAAAAG 427 2148591 AAGGTCGTCCAATGTTAATCATTGCGGAAGATGTTGAAGGGGAAGCTCAAGCAACTCTTG 788 IAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGTTTTGGTG 2148531 TACTAAACAAACTTCGCGGAACATTTAACGTAGTAGCCGTGAAAGCTCCTGGTTTCGGTG 848 AACGCCGTAAAGCTATGCTTGAAGATATTGCTATCCTTACTGGAGGAGAAGCAATATTTG 2149128 AAGACCCATTTGAAAATATGGGAGCAAAACTTGTATCTGAAGTTGCTTCTAAAACCAATG 428 AAATAGCTCAAGTTGGAACCATTTCTGCAAACTCTGATACAACAATAGGTAATATGTAG TIGAAACTACATTAGATGTGGTTGAAGGAATGAAGTTTGACCGTGGCTACCTCTCTCCAT ACTITIGIAACTAATCCTGAGAAATGGTTTGTGAACTTGATAACCCTTATATCCTTTGTA TAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCAACACTTG 908 AAGAICGIGGIAIAAAAGCIIGAAAAIGIAAGCIIGICIICIIIAAGAACAGCIAAAACGIG CTGAAGCTATGGCTAAAGTTGGAAAAGGAGGTGTTATCACAGTTGAGGAAGCTAAAAGGTC TTGCAAATGCTGTTAAAGTAACACTTGGACCTAAAGGCCGTAATGTCGTTATTGAAAAGT 608 668 368 548 488 728 896 89

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                        CTGCTACTGAAACTGAAATGAAAGAAAGAAGGATCGTGTAGAAGATGCTCTAAATGCAA
                                           2148171 CIGCAACIGAAACAGAGCIAAAAGAACGIAAAIIACGIAIIGAAGAIGCACIIAACICIA
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                                                                                          CTCGCGCAGCTGTAGAAGGTATCGTAGCTGGTGGTGGTACTGCCCTTGTAAGTATTT
                                                                                                               TTAAAGTCCTTGATGATATTAAACCTGCTGATGATGAACTTGCTGGACTTAATATCA
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                                                                                                                                                                                                                                                                                                   CATTACAAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGCGCTATTGCTG
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                                                                                                                                                                                                                                                                                                                                               AAAAACCAGAACCTAAAAAAAGATATGCCTATGCCTGGCGGTGGTATGGGTATGGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              open reading frame; ORF; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus influenzae complete genome sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                  2147694 GCATG 2147690
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21-APR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism;
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565350 ATGGCAGCAAAAGACGTAAAATTTGGTAATGACGCACGCGTAAAAATGCTTAAAGGCGTG 565409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        565709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTCTTGTAGATAAAAAATCTCTAACATTCGTGAATTACTTCCCGTGTTAGAAGGCGTT 566069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                    Haemophilus influenzae strain Rd. The invention relates to a computer readable medium (CRM) having recorded upon it the complete H.influenzae nucleotide sequence (I), a representative fragment of (I) or a nucleotide sequence at least 98 identical to (I). By providing the full-length genomic sequence in a computer readable form, it is possible to identify commercially important nucleic acid fragments and expression modulating fragments (EMFs) of the Haemophilus genome. The EMFs can be used to regulate the expression of a nucleic acid molecule. Vectors and altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organisms comprising the predicted ORFS can be used to produce any of the polypeptide fragments of the H. influenzae Rd genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other;
                                                                                                                                                                                                           genome sequence of the bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            565710 GATAAAGCAGTAAGTGCGGTTGTTTCTGAACTTAAAATTTTATCTAAACCTTGTGAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGCCTTCTAAAGAAATCCTTTTTGATGCTAAAAGCCCGTGAAAAACTTTCACGAGGTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GATAAACTIGCAAAIGCIGIIAAAGIAACACTIGGACCIAAAGGCCGIAAIGICGITAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        565410 AATGTATTAGCGGATGCAGTAAAGTAACCCTTGGCCCGAAAGGTCGTCATGTAATTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     565470 GATAAATCATTTGGCGCACCAACTATCACTAAAGACGGGGGGGTGTCTGTTGCTCGTGAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      565530 GAATTAGAAGATAAATTCGAAAACATGGGGGCCACAAATGGTGAAAGAAGTGGCATCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 ACTAGCGATATTGCTGGTGATGGAACTACAACAGCAACAGTCCTTGCACAGGCTATTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 CGTGAAGGTGTAAAACTTGTAGCAGCTGGTCGTAATCCTATGGCCATTAAACGTGGCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               565650 AAridAAGGCTrGAAAGCAGTAGCTGCAGTATGAATCCAATGGATTTAAAACGTGGTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 CAAAAAGAAATAGCTCAAGTTGGAACCATTTCTGCAAACTCTGATACAACAATAGGTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAAAGTCTTTTGGTTCCCCAGTTATTACAAAAGATGGTGTATCTGTTGCAAAAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAACTTGAAGATAAGTTTGAAAATATGGGCGCTCAAATGGTTAAAGGAAGTAGCTCCCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             565770 GCAAAAGAAATIGAACAAGIAGGACIATITICIGCAAACTICIGACAGCATIGIGGGICAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAGGICTIGAAACTACATTAGAIGTGGTTGAAGGAATGAAGTTTGACCGTGGCTACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           565890 ACGGGTCTTGAAGATGAATTAGATGTGGTTGAAGGCATGCAATTAGATAATGGTTACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 ATCATAGCTGAAGCTATGGCTAAAGTTGGAAAAGCAGGTGTTATCACAGTTGAGGAAGCT
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medium - useful for identifying commercially important nucleic acid fragments by homology searching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1830121 BP; 567399 A; 350615 C; 347389 G; 564036 T; 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1830121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 721; DB 17; Length 1
Pred. No. 2e-155;
0; Mismatches 560; Indels
                                                                                                                          English
                                                                                                                                                                                                       This sequence represents the complete
                                                                                                                      Claim 1; Page 77.2-77.1091; 1291pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 43.8%;
Best Local Similarity 65.7%;
Matches 1083; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361
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GCTAAAGTAAACCGTCCACTCCTTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCA

721

Location/Qualifiers

314..622

/*tag= a /label= hypA 673..2307

label= hypB

*tag=

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83..88 /*tag=

120..127 /*tag= d 301..304 Ъ Φ

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Antibodies; heat shock; hypersensitive; allergen; HSP60; GroEL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USSH ) NAT INST OF HEALTH
                                                                      Chlamydia psittaci GPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1991-245693/33
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                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                     misc feature
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 Hyp operon
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                                                                                                                                                                                                                                                                                                                               cerminator
                                           GroES; ss
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 566790 GCAGGAACAGAACAGTACGGCGATATGATCGAAATGGGTATCTTAGATCCAACTAAAGTC 566849
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566070 GCGAAAGCAGGTAAACCGTTATTAATCATCGCTGAAGACGTGGAAGGCGAAGCGCTTGCA 566129
                                                                                                           566190 TITGGTGATCGTCGTAAAGCGATGTTACAAGATATTGCAATTTTAACAGCGGTACAGC 566249
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                             840
                                                                                       TTTGGTGAACGCCGTAAAGCTATGCTTGAAGATATTGCTATCCTTACTGGAGAGAAGCA 900
                                                                                                                                                                                                                                     566310 AAACGIGITIGITATCAATAAAGATAACACAACCATTATTGATGGTATCGGCGATGAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCTC----CATTAAAGTCCTTGATGATATTAAACCTGCTGATGATGATGAACTTGCTGGA
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                                                                                                                                                                             566250 ATTICTGAAGAAATTGGTATGGAGCTTGAAAAAGCAACATTGGAAGATTTAGGTCAAGCA
                                                                                                                                                                                                                                                                      1021 GATATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTAT
                                                                                                                                                                                                                                                                                                                                 1081 GATCGTGAAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       566670 ATCAAACTTGCATTACGTGCTATGGAAGCGCCTTTACGTCAAATCGTCACTAACGCAGGT
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                                                                                                                                                  901 ATAITIGAAGAICGIGGIAIAAAAGCIIGAAAAIGIAAGCIIGICIIIIAGGAACAGCI
                               ACACTTGTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGT
                                                         566130 ACCTTAGTGGTAAACACTATGCGCGGTATCGTGAAAGTTGCAGCCGTGAAAGCACCAGGT
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/*tag= i |label= oligo /note= "used in Northern blot analysis"

/*tag= h /label= oligo /note= "used for Northern blot 2152..2187

/*tag= g
/note=" dyad symmetry;

350..385

/*tag= f 2404..2440

656..659

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US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.)
(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Note: Revised entry submitted to correct the patent number format of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                  The sequence was obtd. from clone pGP57 isolated from a DNA library prepd. from C. psittaci genomic DNA. The two ORFs encode HypA and HypB hypersensitivity proteins, regulated by a heat shock type promoter region. The DNA can be used to produce recombinant pronceins or to design probes for the detection of Chlamydial infection. The Hyp proteins can be used to to raise antibodies and in vaccines. The Hyp B protein elicits a cell-mediated immune response so can be used as a skin test antigen.
DNA encoding HypA and HypB Chlamydia proteins - used to develop prods. for detection of and vaccines against Chlamydia infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.3%; Score 713.6; DB 12; Length 2465; 66.0%; Pred. No. 1.3e-154; tive 0; Mismatches 534; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2465 BP; 853 A; 467 C; 509 G; 636 T; 0 other;
                                                                                                                                    Disclosure; Fig 5; 51pp; English
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AAQ13136 standard; DNA; 2465

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                                                                                                                                                                                                                                     The sequence was obtd, from clone pTA571 isolated from a DNA library prepd. from C. trachomatis genomic DNA. The two ORFs encode HypA and HypB hypersensitivity proteins. The DNA can be used to produce recombinant proteins or to design probes for the detection of Chlamydial infection. The Hyp proteins can be used to to raise antibodies and in vaccines. The Hyp B protein elicits a cellmediated immune response so can be used as a skin test antigen.
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                                                                                                                                              DNA encoding HypA and HypB Chlamydia proteins - used to develop prods. for detection of and vaccines against Chlamydia infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 710.4; DB 12; Length 2223;
Pred. No. 6.9e-154;
0; Mismatches 536; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             web site at www.derwent.com/dwpi/updates/ntis_us.html.
(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2223 BP; 745 A; 408 C; 489 G; 581 T; 0 other;
                                                                                                                                                                                                         Disclosure; Fig 7; 51pp; English
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            90US-0143560
                                                                                                         P-PSDB; AAR13336, AAR13337
                                                (USSH ) NAT INST OF HEALTH
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                                                                                         WPI; 1991-245693/33
                                                                                                                                                                                                                                                                                                                                                                                  See also AAQ13136.
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                                                                                 GCTAAAGTAAACCGTCCACTCCTTATTACTGAAGACGTAGAAGGTGAAGCACTTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                1161 ACTITIGGICGIGAACAGAATITCGIGGAGGATITCCGGGGTITIGCGCAGTITAAAGCTCCAGGC
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                                                                                                                                                                                                                                                   1101 GCTGAATCCGGCCGTCCTCTTATTATAGCAGAAGACATTGAAGGCGAAGCTTTAGCT
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CTTTGTAATGAGAAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTT
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The present invention describes a gene (I) derived from Buchnera sp. containing the DNA (a) or (b), (a) has a fully defined base pair sequence selected from a table of sequences found in the Buchnera sp. genomic DNA of ABA92787 given in the specification or is a DNA selected from complementary DNA sequences, and (b) is a DNA which hybridises with the DNA (a) and encodes a protein. Also described are: (1) a recombinant vector (II) containing (I); (2) a transformant (III) containing (II); (3) a genomic DNA of Buchnera sp. containing the sequence given in ABA92789; (4) a plasmid derived from Buchnera sp. containing DNA (c) or (d), (c) is a DNA containing a fully defined sequence given in ABA92789 ond (d) is a plasmid which hybridises with a DNA; and (5) a method for the preparation of a protein in which (III) is cultured and the expression protein of a protein in which (III) is cultured and resultant culture. The DNA is useful for developing agricultural chemicals for exterminating cockroaches. The present sequence represents the present sequence from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .8955 GCAAACGATGCAGCAGGTGATGGTACCACAACAGCAACATTATTAGCACAATCTATAGTA 19014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 640681 BP; 237522 A; 83822 C; 84757 G; 234580 T; 0 other;
                                                                                                       cockroach-symbiotic bacterium; cockroach extermination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 640681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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4.9e-153;
ches 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic DNA of cockroach-symbiotic bacterium
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43.1%; Score 710; DB
Best Local Similarity 64.5%; Pred. No. 4.9e
Matches 1061; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 16-230; 237pp; Japanese.
                                                                Buchnera sp. genomic DNA SEQ ID NO:1
                                                                                                                                                                                                                                                                                                 07-APR-2000; 2000JP-0107160.
                                                                                                                                                                                                                                                                                                                                           07-APR-2000; 2000JP-0107160.
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                                                                                                                                                                     Buchnera sp.
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361 GATAAAGCTGTTGTTGCTGTTACTAAAGAACTAAGCGACATTACAAAGCCTACTCGTGAC 420
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                                                                                    CAAAAAGAAATAGCTCCAAGTTGGAACCATTTCTGCAAACTCTGATACAATAGGTAAT
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20095 GAACCTTCTGTAGTTACAAACAATGTAAAAGACGGAAAAGGTAACTATGGTTACAATGCA 20154

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GIAACTGACTTGCCTAAAGAAGATAAATCTTCTGATTCTAGTTCTTCTCCAGCAGGAGGA 20334
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                                                                  CGIAITGCATTACAAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGCGCT 1560
GCATCAGGAGAATATGAAGACCTTATTAAAGCTGGTGTCATTGATCCTAAAAAAGTTACA 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 2365589 BP; 765914 A; 415261 C; 420487 G; 763927 T; 0 other;
                             20155 GCTACTGATGATATGGTGACATGATAGATTTTGGTATATTAGATCCAACTAAAGTTACA
                                                                                                                                        1561 ATTGCTGAAAAACCAGAACCTAAAAAAAGATATGCCTATGCCTGGCGGTGGTATGGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleotide sequence useful in the identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.0%; Score 708.4; DB 24; Length 2365589; 66.5%; Pred. No. 1.7e-152; ive 0; Mismatches 521; Indels 6; Gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ehrlich SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic sequence of Lactococcus lactis IL1403
                                                                                                                                                                                                                                                20335 ArgegregeArgegregaArgaTGTA 20360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         production of yogurt and cheese.
                                                                                                                                                                                                                                                                                                                                         DNA; 2365589
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7 TCTAAAGAAATCCTTTTTGATGCTAAAAGCCCGTGAAAAACTTTCACGAGGTGTAGATAAA

Conservative

Matches 1047;

Similarity

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6; Gaps

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CTGTTGTTGCTGTTACTAAAGAACTAAGCGACATTACAAAGCCTACTCGTGACCAAAAG 427
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  fused antigen. Also, where used for cancer control, they lack the side effects associated with endotoxins. They can also be used to detect specific antibodies and in treatment or prevention of tumours (e.g. sarcoma or cancers of breast, overy, prostate, lung, pancreas or liver). The Hsp60 polynucleotide is used for recombinant production of the protein, as a source of primers and probes for detecting streptococci in standard hybridization/amplification assays, and therapeutically in gene therapy vectors.
                                                                                                                                                                                                                                                                                                                                                    CAAAAGAAATCAAATTTTCAGCAGATGCGCGTGCTGCCATGGTGCGCGGAGTTGATATGT
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                                                                                                                                                                                                                               Score 704.2; DB 20; Length 1661; Pred. No. 1.7e-152;
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                                                                                                                                                                                       Sequence 1661 BP; 512 A; 308 C; 407 G; 434 T; 0 other;
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                                                                                                                                                                                                  1327 ATCCGTCGTTCTTGAAGAGCCTTTACGTCAAATTGCTGCAAATGCTGGCTATGAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding a Streptococcus pyogenes heat shock protein (Hsp) 60-2
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856 ATCGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTACAG 915
                                               908 AAGATCGTGGTATAAAGCTTGAAAATGTAAGCTTGTCTTTAGGAACAGCTAAAAGGTG 967
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522 AspLeu-----ProLysLysAspGluGlyMetAlaGlyAlaGlyAspMetGlyGlyMet
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groEL2 chaperonin [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA C;Species: Sinorhizobium meliloti (c;Date: 24-Aug-2001 #text_change 30-Sep-2001 C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001 C;Accession: C95311 Rsharnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows Froc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001 A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11484432

A;Status: preliminary A;Molecule type: DNA

L.; Hyman, R.W.; Jones, T. Schere Solots, T. Schere, 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Reference number: A\$6039; MUID:21368234; PMID:11474104

Genetics

A;Gene: groEL2 A;Genome: plas

C;Superfamily: chaperonin groEL plasmid

> qq ŏ qq à qq

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Conservative: Mismatches: Length: Matches: Indels: 1.13e-94 1864.00 81.24% 70.49% 62.80% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: Pred. No.:

545 387 59 97 6

US-09-077-574A-1 (1-1647) x C95311 (1-545)

Db 361 AspArgGluLysLeuGlnGluAr- Qy 1141 GTTGGAGCTGCTACTGAAACTGA Db 381 ValdlyGlyAlaThrGluValGl Qy 1201 AATGCAACAAGAGCTGGGTTGA Qy 1261 CGCTCCATTAAAGTCCTTGA Qy 1261 CGCTCCATTAAAGTCCTTGA Db 421 ArgSerSerVallysile	A39 VALASTATCATCGTCGTCGTTCTCT 1378 TATGAAGGTTCTATTGTTGTAGA A59 ASPGLIASSETILEVALVAGGA Db 459 ASPGLIASSETILEVALVAGGA Qy 1435 AATGCTGCATCAGGAGAATATGA 10 1435 AATGCTGCATCAGGAGAATATGA 1435 AATGCTGCATCAGGAGAATATGA 1436 AATGCTGCATCAGGAGAATATGA 1437 AATGCTGCATCAGGAGAATATGA 1437 AATGCTGCATCAGGAGAATATGA 1438 AATGCTGCATCAGAGAATATGA 1448 AATGCTGCATCAGAGAATATGA 1448 AATGCTGCATCAGAGAATATGA 1448 AATGCTGCATCAGAGAATATGA 1448 AATGCTGCATCAGAGAATATGAA 1448 AATGCTGCATCAGAATATGAA 1448 AATGCTGCATCAGAATATGAAATATGAAATATGAAATATGAAATATGAAATATGAAATATGAAATATGAAAATATGAAATATGAAATATGAAAATATGAAAATATGAAAATATGAAATATGAAAATATGAAAAAA	1495 499 1555 519 1615	Db 537 GlyGlyMetGlyGlyMetAspMe RESULT 3 UN0509 heat shock protein groEL (clone Rhz P N.Alternate names: chaperonin groEL E C,Species: Rhizobium meliloti C,Date: 31-Dec-1993 #sequence_revisic C,Accession: JN0509 R;Rusanganwa, E.; Gupta, R.S.	Gene 126, 67-75, 1933 Ayritle: Cloning and characterization Ayreference number: JN0509, MUID:9322 Ayreference number: JN0509, MUID:9322 Ayresidues: J-545 cRUS Ayresidues: 1-545 cRUS Ayresidues: Teferences: GB:M94192, NID:g1 C,Comment: This protein plays a role C,Comment: This protein grost A,Gene: großL C,Superfamily: chaperonin großL C,Keywords: heat shock; molecular ch	Alignment Scores:
1 ATGGCTTCTAAAGAAATCCTTTTGATGCTAAAGCCCGTGAAAACTTTCACGAGGTGTA 60 1			541 AAAGGTCTTGAAACTACATTAGATGTGGTTGAAGGAATGAAGTTTGACCGTGGCTACCTC 600 [721 GCTPAAGCTAAACCGTCCACTCCTTATTATTGCTGAAGACGTGAAGGACACTTGCA 780 ::::	901 ATATTTGAAGATCGTGGTATAAAGCTTGAAAATGTAAGCTTGTCTTTAGGAACAGCT 960
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on of multiple groEL chaperonin-encoding genes in Rhiz 231539; PMID:8097179
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e in protein folding and in the extracellular transpor
                                                                                                                                                              SATGATATTAAACCTGCTGATGATGATGAACTTGCTGGA 1317
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                                            AAATGAAAGAAGAAGGATCGTGTAGAAGATGCTCTA 1200
                                                                                                    AAGAAGGIATTGTCCCTGGTGGTGGTACTGCTTTTGTC 1260
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|PheGlyArgSerGlyArgGluLysMetLeuArgGlyVal 20
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Mon Feb

A S S S S S S S S S S S S S S S S S S S	Qy 61 GATAAACTT Db 21 AsplieLell Db 21 AsplieLell Db 41 AsplysSer Qy 121 GAAACTCGAT Qy 241 AsplysSer Qy 241 ACTAGCGAT Qy 361 GATAAAGCT Db 61 GluLeuGlu Qy 361 GATAAAGCT Db 121 AspleuAla Qy 421 CAAAAAGAA Qy 421 CAAAAAGAA Qy 421 CAAAAGAA Qy 541 AAAGGTCTT Qy 541 AAAGGTCTT Qy 541 AAAGGTCTT Qy 541 AAAGGTCTA Qy 781 ACTTCCATA Qy 781 ACTTCCATA Qy 781 ACTTCATAA Qy 781 AAACCTTGTAA Qy 781 AAACCTTGTAA Qy 781 AAACCTTGAA Qy 781 AAAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	DAPATGCTGTTAAAGTAACACTTGGACCTAAAGGCCGTAATGTCGTTATT 1	.LLysValThrLeuGlyProLysGlyArgAsnValVallle 4	TTTGGTTCCCCAGTTATTACAAAAGATGGTGTATCTGTTGCAAAAGAATT 180 ::	3GGCGCTCAAATGGTTAAAGAAGTAGCTCCCAAA 2		ATTGCTGGTGATGGAACTACAACAGCAACAGTCCTTGCACAAGCTATTTAT 300	CATTAAACGTGGCATA 36	7	GITGITGCTGTTACTAAGAACTAAGCGACATTACAAAGCCTACTCGTGAC 420	LeualavalalagluvalvaltysAspieuLeualaiysAlaiysIleAsnThr 140	GGAACCATTTCTGCAAACTCTGATACAACAATAGG	:::	AAAGTTGGAAAAGGAGGTGTTATCACAGTTGAGGAAGCT 54	GlualametGlnLysValGlyAsnGluGlyValIleThrValGluGluAla 180	AAAGGTCTTGAAACTACATTAGATGTGTTGAAGGAATGAAGTTTGACCGTGGCTACCTC 600	GlyTyrLe	TATC 66	roffyrPheValThrAsnProGluLysMetValAlaAspLeuGluAspAlaPheIle 220	GAGAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTT 720	LeuLeuHisGluLysLysLeuSerAsnLeuGlnAlaMetLeuProValLeuGluAlaVal 240	TAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCA 780	GlyLysProLeuLeullelleAlaGluAspValGluGlyGluAlaLeuAla 260	ACACTIGIRGICAATAAGCICCGIGGAGCACTCCAAGTIGIAGCCGIAAAAGCICCIGGI 840	ValAsniysLeuArgGlyGlyLeuLysIleAlaAlaValLysAlaProGly 280	TTTGGTGAACGCCGTAAAGCTATGCTTGAAGATATTGCTATCCTTACTGGAGGAGAAGCA 900	ArgArgLysAlaMetLeuGluAspileAlaileLeuThrGlyGlyThrVal 300	TATTIGAAGAICGIGIAIAAAGCIIGAAAAIGIAAGCIIGICIITIAGGAAGAGCI 960	AspleudiyilelysLeudluserValThrLeuAspMetLeudlyArgAla 320	AAACGTGTAGTTATTGACAAAGAAATACTACTATCGTTGATGGTGCTGGAAAATCAGAA 1020	SerileThrLysGluAsnThrThrileValAspGlyAlaGlyGlnLysSer 340	0 (correctantiticathspixt sec	GATUGIGAAAACTICAAGAACTICTGCAAAACTIGTIGGGGGGGGGAGTAGTGTTATCCAT 1140
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GTTGGAGCTGCTACTGAAACTGAAATGAAAGAAGAAGAAGGATCGTGTAGAAGATGCTCTA 1200
                                                    AATGCAACAAGAGCTGCGGTTGAAGAAGGTATTGTCCCTGGTGGTGGTACTGCTTTTGTC 1260
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             459 AspGluAlaSerIleValValGlyLysIleLeuGluLysAsnThrAspAspPheGlyTyr 478
                                                                                                                                                                                                                                                                                 401 AsnalaThrArgalaAlaValGlnGluGlyIleValProGlyGlyValAlaLeuLeu
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GOKDA chaperonin XF0615 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: F82783
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Asture 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Status: preliminary A; Accession: F82783

A;Molecule type: DNA A;Residues: 1-547 <SIM> A;Cross-references: GB:AE003907; GB:AE003849; NID:g9105484; PIDN:AAF83425.1; GSPDB:GN001 A; Experimental source: strain 9a5c

Risimpson, A.J. G., Rethach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neco, E.; Docerna, C.; El-Dorry, H.; Facincani, A.B.; Ferreira, A.J.S.
submitted to GenBank, June 2000, M.C.; Franca, S.C.; Franco, M.C.; Frohm, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigrr J.D.; Junqueira, M.L.; Madeira, A.M.B.N.; Madeira, A.M.B.N.; Madeira, A.M.B.N.; Matchins, E.M.F.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.E.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. A; Authors: da Silva, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak, A; Tenhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.A; Reference number: A59328

A; Contents: annotation

A, Gene: XF0615 C, Superfamily: chaperonin groEL

Alignment Scores:

1.36e-94

Length:

	1081		401	::: 421 ArgAlaileThrAlaileSerAsnLeuLysGlyAlaAsnGluAspGlnThrHisGlyIle 1321 AATAICATCGTCGTTCTTGAAGAGCCTTTACGTCAAATTGCTGCAAATGCTGCTAGT	Db 441 GlnIleAlaLeuArgAlaMetGluAlaProLeuArgGluIleValAlaAsnAlaGLyGlu 460 Qy 1381 GAAGGTTCTATTGTTGTAGAAAAGGTTCGTGAACCAAAAGATGGTTTTGGATTTAATGCT 1440 Dh 461 Glib-Asse-VallIleI-iaAniAsyaliAsGluGlyLyAsAsbAsnPheGlyTyrAsnAla 480	1441	Qy 1501 CGTATTGCATTACAAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGCGCT 1560 	OY 1561 ATTGCTGAAAAACCAGAACCTAAAAAAGATATGCCTATGCCTGGGGGTGGT 1611	1612 ATGGGTGGTATGGGT 	KESULY 5 B4701 GroEL - Chromatium vinosum C;Species: Chromatium vinosum C;Species: Chromatium vinosum C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999	C; Accession: B47073 R; Perreyra R.G.; Soncini, F.C.; Viale, A.M. J; Bacteriol. 175, 1514-1523, 1993 A; Title: Cloning, characterization, and functional expression in Escherichia coli of characterizations, with coling to be considered to the control of the characterizations.	A; Kererence number: A4/0/3; MOID: 93186/21; FMID: 04**812 A; Accession: B470/33 A; Status: preliminary A; Molecule type: nucleic acid	1-546 <fer chaperc<="" ence="" extra="" ge="" rences:="" th="" y:=""><th>Length:</th><th>:: 1852.50 ent Similarity: 81.02% Local Similarity: 68.25% / Match: 2</th></fer>	Length:	:: 1852.50 ent Similarity: 81.02% Local Similarity: 68.25% / Match: 2
Score: 1862.50 Matches: 366 Percent Similarity: 81.39% Conservative: 80 Best Local Similarity: 66.79% Mismatches: 97 Query Match: 2 Gaps: 2	US-09-077-574A-1 (1-1647) x F82783 (1-547) QY	OY 61 GATAAACTIGCAAAIGCIGTTAAAGTAACACTIGGACCTAAAGGCCGTAATGICGTTATT 120 :::	Oy 121 GAAAAGTCTTTGGTTCCCCAGTTATTACAAAAGATGGTGTATCTGTTGCAAAAGAAATT 180 12.::	Oy 181 GAACTTGAAGATTAGAAAATATGGGCGCTCAAATGGTTAAAGAAGTAGCTCCCAAA 240	81 ThrasnasphisalaglyaspGlyThrThrThralaThrValLeuAlaGlnAlaLeuIle 301 CGTGAAGGTGTAAAACTTGTAGCAGGTGGTCGTAATCCTATGGCCATTAAACGTGGCATA	Db 101 ArgGluGlyCysLysAlaValAlaGlyMethenProMetAspLeuLysArgGlyIle 120 Qy 361 GATAAAGCTTGTTGCTGTTACTAAGAACTAAGGACATTACAAAGCCTACTGTGAC 420		141 481	60	99	661 CTTTGTAATGAGAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTT [::::	Oy 721 GCTAAAGTAAACCGTCCTTATTATTGCTGAAGACGTAGAAGCTGAAGCATTGCA 780	781 ACACTTGTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGT 	Oy 841 TTTGGTGAACGCCGTAAAGCTATGCTTGAAGATATTGCTATCCTTATTGGAGGAGGAGGA 900 [:::	OY 901 ATATTGAAGATCGTGGTATAAAGCTTGAAAATGTAAGCTTGTCTTTTAGGAACAGCT 960

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A;Cross-references: GB:M31918
R;Sampson, J.S.; O'Connor, S.P.; Holloway, B.P.; Plikaytis, B.B.; Carlone, G.M.; Mayer, J. Thfect. Immun. 58, 3154-3157, 1990
A;Title: Nucleotide sequence of htpB, the Legionella pneumophila gene encoding the 58-kii A;Reference number: A41472; MUID:90354095; PMID:2117582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 3-188,'S',190-195,'LIAVH',202-347,'T',349-550 <SAM>
A;Cross-references: GB:M91673; GB:M35149; NID:G149689; PIDN:AAA25298.1; PID:G149690
C;Genetics:
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                                      GATCGTGAAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCAT 1140
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                                                               441 AlaileAlaArgArgAlaMetGluGluProLeuArgGlnIleValAlaAsnAlaGlyGlu 460
341 AspIleLysAlaArgCysGluGlnIleArgAlaGlnValGluGluThrSerSerAspTyr 360
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 15-Oct-1999
C;Accession: A44468; A41472
R;Hoffman, P.S.; Houston, L.; Butler, C.A.
Infect. Immun. 58, 3380-3387, 1990
A;Title: Legionella pneumophila htpAB heat shock operon: nucleotide sequence
A;Reference number: A41468; MUID:90382960; PMID:2205580
                                                                                                                  GTTGGAGCTGCTACTGAAACTGAAATGAAAGAAGAAGAAGATCGTGTAGAAGATGCTCTA
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C;Superfamily: chaperonin groEL
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A,Molecule type: DNA
A,Residues: 1-550 <HOF>
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                                                                                                                                                                                                                                   GAACTTGAAGATAAGTTTGAAAATATGGGCGCTCAAATGGTTAAAAGAAGTAGCTCCCAAA
                                                                                                                                                                                                                                                                                                                       61 GluLeuLysAspLysPheGluAsnMetGlyAlaGlnMetValLysGluValAlaSerLys
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ery Match: 62.16% Indels: 2 Gaps: 1	127 TCTTTTGGTTCCCGGTTATTACAAAGATGGTGTATCTGTTGCAAAAGAAATTGAACTT	GATATTGCTGGTGATGGAACTACAACAACAAGTCCTTGCACAAGCTATTATCGTGAA	367 GCTGTTGTGTGTATGTAAAAACTAAGGGAATTACAAGGCCTATACAAAGCCTAAAAA 260 124 AlaValLeuAlaValThrLySLySLeuGlnAlaMetSerLySProCySLySASpSerLyS 143 124 AlaValLeuAlaValThrLySLySLeuGlnAlaMetSerLySProCySLySASpSerLyS 143 427 GAAATAGCTCAAGTTGGAACCTTTTCTGGAAACTCTGATACAACAAAAGGTAATATGATA 486 144 AlaIleAlaGlnValGlyThrIleSerAlaAsnSerAspGluAlaIleGlyAlaIleTle 163	487 GCTGAAGCTAAAGTTGGAAAAGGAGGTGTTATCACAGTTGAGGAAGCTAAAGGT 546 [607 TACTITGTAACTGAGAAAAGGTITGTGAACTTGATAACCCTTATATCCTTGT 666 [::: :: 204 TyrPheIleAsnAsnGlnGlnAsnMetSerCysGluLeuGluHisProPheIleLeuLeu 223 667 AATGAGAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTTGCTAAA 726 224 ValAspLysLysValSerSerIleArgGluMetLeuSerValLeuGluGlyValAlaLys 243	727 GTAAACCGTCCCTTATTATTGCTGAAGACGTGAAGGTGAAGCACTTGCAACACTT 786 244 SerGlyArgProLeullellelleAlaGluAspValGluGlyGluAlaLeuAlaThrLeu 263 787 GTAGTCAATAAGCTCCGGGAGCACTCCAAGTTGTGCGTAAAGCTCCTGGTTTTGGT 846	847 GAACGCCGTAAAGCTATGCTTGAAGATATTGCTATCCTTACTGGAGGAGAAGCAATATTT 906 :::	304 :::

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                                                                421 ArgSerSerThrLysIle---ThrValLysGlyAlaAsnAspAspGlnGluAlaGlyIle 439
                                                                                                                                                                       500 ValArgThrAlaLeuGlnAsnAlaAlaSerValAlaSerLeuLeulleThrThrGluAla
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                                                                                                                                                                                                                                                                121 GAAAAGTCTTTTGGTTCCCCAGTTATTACAAAAGATGGTGTATCTGTTGCAAAAGAAATT
                                                                                                                                                                                                                                                                                           GAACTTGAAGATAAGTTTGAAAATATGGGCGCTCAAATGGTTAAAGAAGTAGCTCCCAAA
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| 321 LysLysValSerIleSerLysGluAsnThrThrIleValAspGlySerGlyAlaLysThr
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1141 381 1201 401 1261	Oy 1321 AATATCATCATC Db 441 LysLeulle Oy 1381 GAAGGTCT Db 461 GluAlaSer Oy 1441 GCATCAGGA Db 481 AlaThrGly		KASULY 9 S39765 Chaperonin 60 - Coxiell C; Species: Coxiella bur C; Date: 19-Mar-1997 #se C; Accession: S39765 R; Vodkin, M.H.; William J. Bacteriol: 170, 1227 A; Title: A heat shock of A; Reference number: S39 A; Reference number: S39 A; Residues: 1-552 < VOD A; Residues: 1-552 < VOD A; Cross-references: GB: C; Superfamily: chaperon	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: DB:	US-09-077-574A-1 (1-164 QY
61 GATAAACTTGCAAATGCTGTTAAAGTAACCTTGGACCTAAAGGCCGTAATGTCGTTATT 120 12.	241 ACTAGCGATATTGCTGGTGAACTACAACAGCAACAGCTCCTTGCACAAGCTATTTAT 300	CAAAAGAATAGCTCAAGTTGGAACCATTCTGCAAACTCTGATACAACAATAGGTAAT SerlysGluileAlaGluValGlySer!	601 TCTCCATACTTGTAACTAATCCTGAGAAAATGGTTTGTGAACCTGATAACCCTTATTTC 660 [::::::::::	841 TTTGGTGAACGCGTAAAGCTAGAAGATATTGCTATCCTTACTGGAGGAGAAGCA 900	961 AAACGTGTAGTTATTGACAAAGAAATACTACTATCGTTGATGGTGCTGGAAAATCAGAA 1020
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	oy Oy	1201 AATGCAAC ::: 401 HisAlaTh:	AAGAGCTGCGGTTGA rArgAlaAlaValGl	AGAAGGTATTGTCCCT(::: uGluGlyValValPro(AATGCAACAAGAGCTGCGGTTGAAGAAGGTATTGTCCCTGGTGGTGGTGGTTTTGTC :::	1260 420
	<u>م</u> م	1261 CGCTCCAT	TAAAGTCCTTGATGA ::: :::sGlnAlaIleThrGl	TATTAAACCTGCTGAT(::: ::: vLeuLysGlyAspThr)	GGCTCCATTAAAGTCCTTGATGATATTAAACCTGCTGATGATGATGAACTTGCTGGACTT	1320
	, AO 1		CCGTCGTTCTTCA	AGAGCCTTTACGTCAA	AATATCATCCGTCGTTCTCTTGAAGAGCCTTTACGTCAAATTGCTGCAAATGCTGGCTAT	1380
	g ò	1381 GAAGGTIC	ereuargaravalei TATTGTTGTAGAAAA	ugiurioleuaigini. Agttcgtgaaccaaaa		1440
	QQ QQ		::: rvalvalvalAsnTh	 rValLeuAsnGlyLys	:::	480
	<u>ک</u> ج	1441 GCATCAGG ::: 481 AlaThrel	AGAATATGAAGACCT vG]uTvrG]vAspLe	TATTAAAGCTGGTGTC ::::: wyalGluGlnGlvyal	GCATCAGGAGAATATGAAGACCTTATTAAAGCTGGTGTCATTGATCCTAAAAAAGTTACA	1500
	ì à		ATTACAAAATGCAGC	ATCAGTAGCCTCCTTA		1560
	qq	501 ArgThrAl				520
	٥٧		AA	accagaacctaaaaaa 	ATGCCTGGC	1608
	Ωp	521 ValValGl	uLeuMetGluAsnLy	ValValGluLeuMetGluAsnLysProAlaAlaAlaProAlaMetPro	AlaMetProGly	537
	\text{\delta} \frac{\text{\delta}}{\text{\delta}}	1609 GGTATGGG 538 GlyMetGl	GGTATGGCTGCTATGGCTGGTATGGAC	GGAC 1635 tAsp 546		
	RESULT 9 S39765 chaperon C;Species C;Date:	in 60 - Coxiel s: Coxiella bu 19-Mar-1997 #s	la burmetii krnetii equence_revisio	n 25-Apr-1997 #t	ext_change 28-May-1999	
	C; Access R; Vodkin J. Bacte	ion: S39765 1, M.H.; Willia riol. 170, 122	ms, J.C. 77-1234, 1988	C; Accession: S39765 R; Vodkin, M.H.; Williams, J.C. Bacteriol. 170, 1227-1234, 1988	discos a maior antigon	ന്നതി വരവുടെ 10
	A; Access A; Status A; Molecu	A;ILLE: A Hear SHOCK O A;Reference number: S39 A;Accession: S39765 A;Status: preliminary A;Molecule type: DNA	9764; MUID:8813	19182; PMID:33432		
_	A;Residu A;Cross- C;Superf	les: 1-552 <vod references: GB amily: chapero</vod)> }:M20482; NID:g1 nin groEL	A;Residues: 1-552 <vod> A;Cross-references: GB:M20482; NID:g144996; PIDN:AAA23309 C;Superfamily: chaperonin groEL</vod>	3309.1; PID:g144998	
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	AQ	1 ATGGCTTC : 1 MetAlaAl	TAAAGAAATCCTTT7 aLysValLeuLysPt	rrgargcraaagcccgr 	AIGGCTICTAAAGAAAICCITITIGAIGCTAAAGCCCGTGAAAAACTITCACGAGGTGTA ::: 	60 20
	yy Dp	61 GATAAACT ::: 21 GluValLe	TGCAAATGCTGTTAA 	AGTAACACTTGGACCT 	GATAAACTTGCAAATGCTGTTAAAGTAACACTTGGACCTAAAGGCCGTAATGTCGTTATT :::	120 40
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AsplysSerPheGlyAlaProThrIleThrLysAspGlyValSerValAlaLysGluIle 60 GAACTTGAAGATAAGTTGAAAATATGGGGGCTCAAATGGTTAAAGAAGTAGCTCCCAAA 240 G	ACTAGCGATATIGCTGGTGATGGAACTACAACAGCAACAGTCCTTGCACAAGCTATTTAT 300 	CGTGAAGGTGTAAAACTTGTAGCAGCTGGTCGTAATCCTATGGCCATTAAACGTGGCATA 360 :::	GATAAAGCTGTTGTTGCTAACAACTAAGGACATTACAAAGCTACTCGTGAC 420 	CAAAAAGAAATAGCTCAAGTTGGAACCATTTCTGCAAACTGATACAACAATAGGTAAT 480 	ATCATAGCTGAAGCTATGGCTAAAGGTTGGAAAAGGGGGTGTTATCACAGTTGAGGAAGCT 540 	AAAGGTCTTGAAACTACATTAGATGTGGTTGAAGGAATGAAGTTTGACCGTGGCTACCTC 600	TCTCCAFACTITGTAACTAATCCTGAGAAAATGGTTTGTGAACTTGATAACCCTTATATC 660	CTTTGTAATGAGAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTT 720	GCTAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCA 780 	ACACTIGIAGICCAATAAGCICCGIGGAGCACICCAAGIIGIAGCCGIAAAAGCICCIGGI 840 	TTTGGTGAACGCCGTAAAGCTATGCTTGGTATCTTACTGGAGGAGAAGCA 900 :::	ATATITGAAGATCGTGGTATAAAGCTTGAAAATGTAAGCTTGTCTTTAGGAACAGCT 960 	AAACGIGIAGTIATIGACAAAAAAAATACIACIATCGITGGIGGGGAAAAICAGAA 1020 ::: LysArgValValValThrLysAspAspThrThrIleIleAspGlySerGlyAspAlaGly 340		GATCGTGAAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCAT 1140 :::	니 4	12
41 181 61	241	301	361	421	161	541 i81	601	661	721	781	841	301	961	1021	1081	1141	1201
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probable heat shock protein groEL [imported] - Sinorhizobium meliloti (strain 1021) maga C;Species: Sinorhizobium meliloti (Species: Sinorhizobium meliloti (Species: Sinorhizobium meliloti (Species: Sinorhizobium meliloti (Species: Sinorhizobium meliloti (Spacession: F9567)

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar Proc. Natl. Acad. Sci. US.A. 98, 9889-9894, 2001

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar Proc. Natl. Accession: F9567

A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endch A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Residues: 1-542 cKUR>
A;Reference 3: 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A;Authors: Kahn, D.; Kahn, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.; A;Charents: annotextion
A;Reference number: A96039; WUID:21368234; PMID:111474104
1261 CGCTCCATTAAAGTCCTTGATGATATTAAACCTGCTGATGATGATGAACTTGCTGGACTT 1320
                                                                                                               1321 AATATCATCCGTCGTTCTCTTGAAGAGCCTTTACGTCAAATTGCTGCAAATGCTGGCTAT 1380
                                                                                                                                                                                                                           1381 GAAGGTTCTATTGTTGTAGAAAAGTTCGTGAACCAAAAGAT---GGTTTTGGATTTAAT 1437
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                                                                                                                                                     441 GlulleAlaArgArgAlaMetAlaTyrProLeuSerGlnIleValLysAsnThrGlyVal
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A,Genome: plasmid
C,Superfamily: chaperonin groEL
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Page 11

		RESULT 11 AD2660 60 KDA chaperonin [imported] - Agrobac C; Species: Agrobacterium tumefaciens C; Date: 11-Jan-2002 #sequence_revision C; Accession: AD2660 R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A; Authors: Yoo, H.; Tao, Y.; Biddle, P. Ster, E.W. A; Authors: Yoo, H.; Tao, Y.; Biddle, P. Ster, E.W. A; Authors: Yoo, H.; Tao, Y.; Biddle, P. Ster, E.W. A; Reference number: AB2577; MUD:21608 A; Reference number: AB2577; MUD:21608 A; Redus: prelliminary A; Molecule type: DNA A; Roberimental source: strain C58 (Dup. C; Genetics: A; Gene: groEL A; Map position: circular chromosome C; Superfamily: chaperonin groEL	Alignment Scores: Pred. No.: Score: Score: Score: Bercent Similarity: Best Local Similarity: 62.01% Ouery Match: DB: US-09-077-574A-1 (1-1647) x AD2660 (1-000) QY 1 ATGGCTTCTAAAGAAATCCTTTTTTTTTTTTTTTTTTTT
61 GATAAACTTGCAAATGCTGTTAAAGTAACACTTGGACCTAAAGGCCGTAATGTCGTTATT 120 21 ASPVAlLeuAlaASanAlaValLysValThrLeuGlyProLysGlyArgAsnValValIle 40 121 GAAAAGTCTTTTGGTTCCCCAGTTATTACAAAAGATGGTGTATCTGTTGCAAAAGAAATT 180 :::	101 Argcludtyalaiysalavallaiseriliymetasnprometaspieurysargciyili 120 361 GATAAAGCTGTTGTTGCTGTACTAAAGACTAAGCGACATTACAAAGCCTACTCGTGAC 420 121 AspleuAlavalAspalavalvallysGluLeuLysasnAsnalaArgLysIleSerLys 140 421 CAAAAGAAATAGGTCAAGTTGGAACTTCTGCAAACTCTGATACAATAGGTAAT 480 141 AsnSerGlulleAlaGlnValGlyThrIleSerAlaAsnGlyAspThrGlulleGlyArg 160 481 ATCATAGGTGAAGCTAAAGTTGGAAAAGGAGGGGTTATCACAGTTGAGGAAGCT 540 15::	TCTCCATACTTTGTAACTAATCCTGAGAAATGGTTTGTGAACTTGATAACCCTTATATC	961 AAACGTGTAGTTATTGACAAAATACTACTATTGGTGGTGCTGGAAAATCAGAA 1020 321 [::
6 6 6 6 6 6 6 6	8 6 8 6 8 6 8		6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6

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P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     netic Engineer Agrobacterium tumefaciens C58. 08550; PMID:11743193
                                                        AGAAGGTATTGTCCCTGGTGGTGGTACTGCTTTTGTC 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAAAAAAGATATGCCTATGCCTGGCGGTGGTATGGGT 1617
                                                                                                                                   TATTAAACCIGCIGAIGAIGAIGAACTIGCIGGACTI 1320
                                                                                                                                                                                                             AGAGCCTTTACGTCAAATTGCTGCAAATGCTGGCTAT 1380
                                                                                                                                                                                                                                                                                  AGTICGIGAACCAAAGAI---GGITTIGGAITTAAI 1437
                                                                                                                                                                                                                                                                                                                                                            CCTTATTAAAGCTGGTGTCATTGATCCTAAAAAGTT 1497
                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGC 1557
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yLeuLysThrAlaAsnAsnAspGlnArgValGlyVal 440
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sGluAlaAlaProAlaLeuProAlaGly------ 537
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Matches:
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60K chaperonin (protein cpn60) (groEL protein) [imported] - Agrobacterium tumefaciens (sc)Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Accession: B97442
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wolllam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2332-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
1141 GTTGGAGCTGCTACTGAAACTGAAATGAAAGAGAAGGATCGTGTAGAAGATGCTCTA 1200
                                                                                      AATGCAACAAGAGCTGCGGTTGAAGAAGGTATTGTCCCTGGTGGTGGTACTGCTTTTGTC 1260
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                         A;Accession: B97442
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-544 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK86491.1; PID:g15155641; GSPDB:GN00169
C;Genetics:
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A;Status: preliminary
A;Molecule type: DNA
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                     GAAAAGTCTTTTGGTTCCCCAGTTATTACAAAAGATGGTGTATCTGTTGCAAAAGAAATT
                                 GAACTIGAAGATAAGTTTGAAAATATGGGCGCTCAAATGGTTAAAGAAGTAGCTCCCAAA
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groEL protein - Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C;Accession: S23918
R;Segal, G.; Ron, E.Z.
submitted to the EMBL Data Library, August 1992
A;Description: Cloning and sequencing of the GroE operon of Agrobacterium tumefaciens C58
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AATGCAACAAGAGCTGCGGTTGAAGAAGGTATTGTCCCTGGTGGTGGTACTGCTTTTGTC 1260
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A;Cross-references: EMBL:X68263; NID:g1019913; PIDN:CAA48331.1; PID:g39095
C;Superfamily: chaperonin groEL
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                     CGCTCCATTAAAGTCCTTGATGATATTAAACCTGCTGATGATGATGAACTTGCTGGACTT
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42	132	44(1381	46(1438	48(1498	. 20(1558	52(161	54(LT 14 98	C;Species: Ps	C, Mare: 13-36 C, Accession:	k;Stover, C.P adman, S.; Yu	ory, S.; re 406, 9	tle: Comp ference r	cession: atus: pre	lecule ty sidues: 1	oss-refer perimenta	C;Genetics: A;Gene: groEI	perfamily	Alignment Sco Pred. No.:	core: ercent Simil	Best Local Si Query Match:		US-09-077-574	1	П	61	21	121	41	181	61
ପ୍ପ	δλ	Dp	δλ	qq	δλ	QO	Qy	ΩÞ	ΟŊ	Dp	δλ	Op	RESULT B83098	GS.C	C; Ac	R;St adma	Natu	A;Ti A;Re	A; Ac	A; Mo	A; Cr. A; Exj	C;Gel A;Gel	C;Suj	Aligr	Score:	Best	DB:	US-0	QY	q	δλ	qq	δλ	qq	ò	qa
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61 Gluleugluasplysphegluaspmerglyalagluleniyalayogluyalalaseriya 80	ACTAGCGATATTGCTGGTGATGGAATTACAACAACAACAACAACAACAACAACAACAACAACA	ThrasnaspilealadjyaspGlyThrThrThrAlaThrValleuAlaGlnAlaIleVal		ArgGluGlyAlaLysAlaValAlaAlaGlyMetAsnProMetAsDLeuivsArgGlyIle	GATAAAAGCTGTTGCTGTTACTAAAAGAACTAAAGGCGACATTACAAAAGCTGAAAAGCAAAAAGCTGAAAAAAAA		ларыссатакатыластакаткаткаты экип жарыссаны жарын апуытын түрктений жарын жары	SerGluGluValAlaGlnValGlyThrileSerAlaAsnGlvGluAraGlnIleGlyLeu		AsplieAlaGluAlaMetGluArdValGlyAsnGluGlyValIleThrValGluGluAla		181 LysThrAlaGluThrGluLeuGluValValGluGlyMetGlnPheAspArgGlyTyrLeu 200		201 SerProTyrPheValThrAsnProGluLysMetValAlaAspLeuGluAspAlaTyrIle 220	661 CITIGIAAIGAGAAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTT 720	221 LeuLeuHisGluLysLysLeuSerAsnLeuGlnAlaMetLeuProValLeuGluAlaVal 240	721 GCTAAAGTAAACCGTCCACTCCTTATTGCTGAAGACGTGAAGGTGAAGCACTTGCA 780	241 ValGlnThrClyLysProLeuValIleIleAlaGluAspValGluGlyGluArgLeuAla 260	781 ACACTTGTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGT 840	261 ThrLeuValValAsnLysLeuArgGlyGlyLeuLysIleAlaAlaValLysAlaProGly 280	841 TITGGTGAACGCCGTAAAGCTATGCTTGAAGATATTGCTATCCTTACTGGAGGAGAAGCA 900	281 PhedlyAspArgArgLysAlaMetLeuGluAspIleAlaileLeuThrGlyGlyThrVal 300	901 ATAITIGAAGAICGIGGIAIAAAGCIIGAAAAIGIAAGCIIGICIICIIIAGGAACAGCI 960	301 IleSerGluAspLeuGlyIleLysLeuGluSerValThrLeuAspMetLeuGlyIysSer 320	961 AAACGTGTAGTTATTGACAAAGAAAATACTATCGTTGATGGTGCTGGAAAATCAGAA 1020	:::	1021 GATATTAAAGCTCGAGTTAAAGAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTAT 1080	341 AspileGluGlyArgValAlaGlnileLysAlaGlnileGluGluThrThrSerAspTyr 360	1081 GATCGTGAAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCAT 1140	361 ASPArgGluLysLeuGlnGluArgLeuAlaLysLeuAlaGlyGlyValAlaVallleArg 380	1141 GTTGGAGCTGCTACTGAAACTGAAATGAAAGAGAAGAAGGATCGTGTAGAAGATGCTCTA 1200		1201 AATGCAACAAGAGCTGCGGTTGAAGAAGGTATTGTCCCTGGTGGTGGTACTGCTTTTGTC 1260		1261 CGCTCCAFTAAAGTCCFTGATGATATTAAACCTGCTGATGATGATGAACTTGCTGGACTT 1320	
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Pseudomonas aeruginosa
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Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
S.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br. Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, 959-964, 2000
mplete ganome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathornumber: A82950; MUID:20437337; PMID:109840643
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tal source: strain PA01
                                                   21 AATATCATCCGTCGTTCTTCTTTGAAGAGCCTTTACGTCAAATTGCTGCAAATGCTGGCTAT 1380
                                                                                                                                                           81 GAAGGTTCTATTGTTGTAGAAAAGTTCGTGAACCA---AAAGATGGTTTTGGATTTAAT 1437
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| AsnileValArgiysAlaLeuGinSerLeuValArgGinIleAlaGluAsnAlaGlyAsp 459
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| MetAlaAlabJysGluValLysPheGlyAspSerAlaArgLysNetLeuValGlyVal
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C,Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 26-Aug-1999
C,Accession: S22347
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C;Superfamily: chaperonin groEL
                                                         GAAGGTTCTATTGTTGTAGAAAAAGTTCGTGAACCAAAAGATGGTTTTGGATTTAATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                         R.Gor, D.; Mayfield, J.E.
Biochim. Biophys. Acta 1130, 120-122, 1992
A.Title: Cloning and nucleotide sequence of the Brucella abortus grob (A.Reference number: S22346; MUID:92182006; PMID:1347461
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	AGCTGTTGTTGCTGTTACTAAAGACTAAGGGGCATTACAAGCCTACTCGTGAC 42	
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421	CAAAAACAAATAGCTCAAGTTGGAACCATTTCTGCAAACTCTGATACAACAATAGGTAAT 480 ::: :::	
481		
541	AAAGGTCTTGAAACTACATTAGATGGGTTGAAGGAATGAAGTTTGACCGTGGCTACCTC 600 	
601	TCTCCATACTTTGTAACTAATCCTGAGAAAATGGTTTGTGAACTTGATAACCCTTATATC 660	
661	CTTTGTAATGAGAAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTT 720 ::: 	
721	GCTAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCA 780 ::: ::::	
781	ACACTTGTAGTCAATAAGCTCCGGGGGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGT 840 	
841	TTTGGTGAACGCCGTAAAGCTATGCTTGAAGATATTGCTATCCTTACTGGAGAGAAGCA 900 :::	
301	ATATTIGAAGAICGIGGTATAAAGCTIGAAAAIGTAAGCTIGICTITAGGAACAGCT 960 	
961	AAACGIGTAGTIATIGACAAAGAAAATACTATGGTIGATGGTIGCTGGAAAATCAGAA 1020 :::	
1021	GATATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTAT 1080 :::	
1081	GATCGTGAAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCAT 1140 	
1141	GTTGGAGCTGCTACTGAAACTGAAATGAAAGAAGGAACGATCGTGTAGAAGATGCTCTA 1200 	
1201	AATGGAACAAGAGCTGGGGTTGAAGAGGTATTGTCCCTGGTGGTACTGCTTTTGTC 1260	
1261	CGCTCCATTAAAGTCTTGATGATATTAAACCTGCTGATGATGAAGAAGAACTTGCTGGA 1317 	
1318	h ::d	
1378	TATGAAGGTTCTATTGTAGAAAAGTTCGTGAACCAAAAGATGGTTTTGGATTT 1434	

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Search completed: January 28, 2004, 13:30:02 Job time : 57.5 secs

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BLOSUM62 Kgapop 10.0 , Kgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext

US-09-077-574A-1

2968

score:

Sequence: Title: Perfect

OM nucleic

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Scoring table:

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Sequence 17524, Application US/10369493

Publication No. US20030233675A1

GENERAL INPORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52022) B
CURRENT APPLICATION WUMBER: US 40)360,039

PRIOR FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

LENGTH: 547
Sequence 17524, A Sequence 10014, A Sequence 11760, A Sequence 10295, A Sequence 16295, A Sequence 15267, A Sequence 15267, A Sequence 15267, A Sequence 15267, A Sequence 15330, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 51, Appl
Sequence 18994, A
Sequence 5, Appli
Sequence 8322, Ap
Sequence 11465, A
Sequence 2550, Ap
Sequence 12526, A
Sequence 20276, A
                                                                                                                                                                                                                                                                                                                                                                    Sequence 12170, A Sequence 12170, A Sequence 1732, A Sequence 11916, A Sequence 4511, Ap Sequence 7269, Application of the Sequence 2, Application of the Sequence 10, Application of the Sequence 10, Application of the Sequence 10662, A Sequence 9597, Application of the Sequence 418, Application of the Sequence 410, Application o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 513, App
Sequence 153, App
Sequence 17907, A
Sequence 20184, A
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                         US-10-369-493-10014

US-10-369-493-11760

US-10-369-493-10760

US-10-369-493-10295

US-10-369-493-10295

US-10-369-493-10546

US-10-369-493-10546

US-10-369-493-10525

US-10-369-493-11525

US-10-369-493-11522

US-10-369-493-1132

US-10-369-493-12170

US-10-369-493-12170

US-10-369-493-12170

US-10-369-493-12170

US-10-369-493-121916

US-10-369-493-121916

US-10-369-493-1269

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US-10-369-493-1269

US-10-369-493-13181

US-10-369-493-13181

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US-10-369-493-13181

US-09-811-132-400

US-09-811-132-400

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US-10-369-493-17907
US-10-369-493-20184
US-10-267-311-51
US-10-369-493-18994
US-10-369-493-18994
US-10-369-493-493-20276
US-10-156-761-11465
US-10-156-761-125-26
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; ORGANISM: Xylella fastidiosa
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US-10-369-493-17524
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                                                                                                                                                                                                                                   January 28, 2004, 13:28:52; Search time 60.5 Seconds
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*

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                                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                          protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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APPLICANT: Gladman, Barry S.
APPLICANT: Gladman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPERSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPERSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US, 10/369, 493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360, 039
PRIOR PLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10014
                 961 AAACGTGTAGTTATTGACAAAGAAATACTACTATCGTTGATGGTGCTGGAAAATCAGAA 1020
                                                                                                                                            GATCGTGAAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCAT 1140
                                                                                                                                                                                                                                                                                                                                  CGCTCCATTAAAGTCCTTGATGATATTAAACCTGCTGATGATGATGAACTTGCTGGACTT 1320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGTATTGCATTACAAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGCGCT 1560
                                                                                                341 AlaileAsnGlyArgValLySGlnIleLySThrGlnIleGluGluThrThrSerAspTyr 360
                                                                                                                                                              1561 ATTGCTGAAAAACCAGAACCTAAAAAAGATATGCCTATGCCT-----GGCGGTGGT 1611
                                                                                                                                                                                                                            401 LeuAlaThrArgAlaAlaValGluGluGlyValIleProGlyGlyGlyValAlaLeuIle 420
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                                                                                1021 GATATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAACAAGCTCAGATTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1441 GCATCAGGAGAATATGAAGACCTTATTAAAGCTGGTGTCATTGATCCTAAAAAGTTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: magnetite-containing magnetic coccus
US-10-369-493-10014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1612 ATGGGTGGTATGGGTGTATGGAC 1635
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Publication No. US20030233675A1
GRNERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-10-369-493-10014
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APPLICANT: Gao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianteng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN 17 TILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR ETLING DATE: 2002-02-21
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                    Matches:
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Sequence 7917, Application US/10369493

Sequence 7917, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei

APPLICANT: Gladman, Barry S.
APPLICANT: Gladman, Barry S.
APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERIES
TITLE OF INVENTION: B-1052052)

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 7917
AAACGTGTAGTTATTGACAAAGAAATACTACTATCGTTGATGGTGCTGGAAAATCAGAA 1020
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      Length:
Matches:
Conservative:
Mismatches:
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                                                                                  US-09-077-574A-1 (1-1647) x US-10-369-493-7917 (1-547)
       4.95e-142
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; Publication No. US20030233675A1
; GENERAL INFORMATION
; APPLICANT: GLO, YONGWei
APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Stewen C.
; APPLICANT: Glater, Stewen C.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN J.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
; FILE REFERENCE: 38-10(52052)
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT PILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 10295
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US-10-369-493-10295
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US-10-369-493-10295
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                    322 IleAsnIleAspLysAspAsnThrThrValValAsnGlySerGlyLeuLysAspAsnIle 341
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|22 AlaValSerAlaIleIleAlaAspLeuLysValGlnSerLysLysIleSerAsnSerAsn 141
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APPLICANT: Cao, Yongwei
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APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 15468
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                 .021 GATATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTAT 1080
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521 ValAlaGlu-----AlaProLysLysAspGluProThrProProAlaAlaGlyGlyGly 538
                                       341 AlaileAsnGlyArgValLysGlnileLysThrGlnileGluGluThrThrSerAspTyr
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                                                                                                              1 ATGGCTTCTAAAGAAATCCTTTTTGATGCTAAAGCCCGTGAAAAACTTTCACGAGGTGTA
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 101
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Mismatches:
Indels:
66.30%
61.79%
 Similarity:
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QY 1021 GATATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTAT 1080 Db 341 ThrIleGluAlaArgValGlyGlnIleLysThrGlnIleGluAspThrSerSerAspTyr 360 QY 1081 GATCGTGAAAAACTTCAAGAACGTCTTGCAGAACTTGTTGGTGGAGTAGCTGTTATCCAT 1140 Db 361 AspArgGluLysLeuGlnGluArgValAlaLysLeuAlaGlyGlyValAlaUsulaGlyGlyValAlaCysLeuAlaGlyGlyValAlaCysLeuAlaGlyGlyGlyCTGTAAAAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Oy 1201 AATGCAACAAGAGCTGCGGTTGAAGAAGGTATTGTCCCTGGTGGTGGTTGTCTTTTTTC 1260 :::		Qy 1501 CGTATTGCATTACAAATGCAGCATCAGTAGCTCCTTACTTA	RESULT 8 US-10-369-493-16217 Sequence 16217, Application US/10369493 Publication No. US2003023367541 Publication No. US2003023367541 APPLICANT: Cao, Yongwei APPLICANT: Slater, Steven C. APPLICANT: Goldman, Barry S. APPLICANT: Chen, Xianfeng TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION C. TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B	CURRENT APPLICATION WUMBER: US/10/369,493
Best Local Similarity: 66.85% Mismatches: 95 Query Match: 12 61.76% Indels: 4 DB: 12 Gaps: 3 US-09-077-574A-I (1-1647) x US-10-369-493-15468 (1-544) QY 1 ATGGCTTCTAAAGAAATCCTTTTTGATGCTAAAGCCGTGAAAACTTTCACGAGGTCTA 60		Oy 241 ACTAGCATATTGCTGGTGATGCAACAACAAGGCAACAGTGCTTGCACAAGTATTTTT 300 B1 ThrashaphanalaGlyAsGlyTh[T][][][][][][][][][][][][][][][][][][421 CAAAAGAAATAGCTCAAGTTGGAACCATTCTGCAAACTCTGATACAATAGGTAAT 421 CAAAAAGAAATAGCTCAAGTTGGAACCATTCTGCAAACTCTGATACAACAATAGGTAAT 141 AsplysAlaileAlaGlnValGlyThrIleSerAlaSnSerAspGluSerIleGlyAsn 481 ATCATAGCTGAACTAGAAAAGGTGGAAAAAGGAGTTGAAGCT	181 SerGlyLeuGluAsnGluLeuAspValValGluGlyMetGlnPheAspArgGlyTyrLeu 601 TCTCCATACTTGTAACTAATCCTGAGAAAATGGTTTGTGAACTTGATAACCCTTATATC 201 SerProTyrPheileAsnAsnGlnGlnSerGlnSerAlaAspLeuAspAspProPheile 661 CTTTGTAATGGAAAAAGATTACTAGCATGAAAGATGCTACCAATCTTAGAACATGT 221 LeuLeuHisAspLysLieSerAsnValArgAspLeuLeuProValLeuGluGlyVal 721 GCTAAAGTAAACGTCCACTCCTTATTATTGCTGAAGAGCGTAGAAGAGACTTGCA 721 GCTAAAGTAAACGTCCACTCCTTATTATTGCTGAAGAGCGTAGAAGCACTTGCA 721 GLTAAAGTAAACTACTATTATTGCTGAAGACGTAGAAGCACTTGCA 721 GLTAAAGTAAACTACTATTATTGCTGAAGACGTAGAAGCACTTGCA 721 AlalysAlaGlyLySProLeuLeuileValAlaGluGluValGluGlyGluAlaLeuAla	Oy 781 ACACTTGRAGTCAATAAGTCCGTGAACACTCCAAGTTGTAGCCGTAAAAGTCCCTGGT 840 261 Thille

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	TTTCACGAGG	STAATGTCGT	 rgAsnValVa	rrgcaaaaga alalarysgl	AAGTAGCTCC uValAlaSe	CACAAGCTAT :: aGlnAlaLe	TTAAACGTGG :: euLysArgGl	AGCCTACTCG ysprothrth	CAACAATAGG ::: luSerIleGl	CAGTTGAGGA hrValGluGl	ACCGTGGCTA spargGlyTy	ATAACCCTTA ::: :: spaspProPh	TCTTAGAACA :: alLeuGluGl	GTGAAGCACT 1yGluAlaLe	TAAAAGCTCC allysalaPr	CTGGAGGAGA hrGlyGlyTh	CTTTAGGAAC spLeuGlyA1	AAACGTGTAGTTATTGACAAAGAAATTCTACTATCGTTGATGGTGCTGGTAAAATCAGAA
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7	CCTTTTGA	TGTTAAAGT	 aValLysAla	CCCAGTTAT:	TGAAAATATC eGluAsnMet	TGATGGAAC yAspGlyThi	TGTAGCAGC	TGTTACTAA) aAlaValil	AGTTGGAAC nvalGlyTh	GGCTAAAGT	ATTAGATGT uLeuAspVa	TAATCCTGA(:: nAsnGlnGl	GATTACTAG ::::: rslleSerAs:	ACTCCTTAT	GCTCCGTGG ::: rrleArgGl	AGCTATGCT rsAlaMetLe	FTATAAAGCT ::: YLeuAlaLe	ACAAAGAAAA
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<i>y</i> Match: 9-077-5748-1 (1-1			21	121	181	241	301	361	421	481	541	601	661	721	781	841	301	1961
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1021 GATATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTAT 1080 -::	1081 GATCGTGAAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCAT 1140 	1141 GTTGGAGCTGCTACTGAAACTGAAAGAGAAGAAGGATCGTGTAGAAGATGCTCTA 1200 	1201 AATGCAACAAGAGCTGCGGTTGAAGAAGGTATTGTCCCTGGTGGTGGTACTGCTTTTGTC 1260 :::	1261 CGCTCCATTAAAGTCCTGATATTAAACCTGGTGATGATGATGAACTTGCTGGACTT 1320	1321 AATAICATCCGTCGTTCTTGAAGAGCCTTTACGTCAAATGCTGCAAATGCTGGCTAT 1380	1381 GAAGGTTCTATTGTAGAAAAAGTTCGTGAACCAAAAGATGGTTTTGGATTTAATGCT 1440 ::::	1441 GCATCAGGAGAATATGAAGACCTTATTAAAGCTGGTGATCATTGATCCTAAAAAAGTTACA 1500 	1501 CGTATTGCATTACAAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGCGCT 1560	1561 ATTGCTGAAAAACCAGAACCTAAAAAAGATATGCCTATGCCTGGCGGTGGTATG 1614 ::: :::	1615 GGTGGTATGGGGGGGTGTATG 1632 	SEGULT 9 SGQUENCE 15265 Sequence 15265, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION: APPLICANT: Cao, Yongwei APPLICANT: Gaiter, Steven C. APPLICANT: Goldman, Barry S. APPLICANT: Goldman, Barry S. APPLICANT: Chen, Xianteng TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)8 FILE REPRENENCE: 38-10(52052)8 CURRENT FILING DATE: 2003-02-28 FRIOR PLILOM ONTES: 2003-02-21 NUMBER OF SEQ ID NOS: 47374 SEQ ID NO 15265 LEMGTH: 543 TYPE: PRT CREATER FILE SECTION NUMBER: US (0/360,039) FRIOR FILING DATE: 2002-02-11 NUMBER OF SEQ ID NOS: 47374 SEQ ID NO 15265 LEMGTH: 543 TYPE: PRT CREATER FILE SET SECTION THREFACE SEG ID NOS: 47374 SEQ ID NO 15265 THENGTH: 543 TYPE: PRT CREATER FILE SECTION THREFACE SEG ID NOS: 47374 TYPE: PRT CREATER FILE SECTION THREFACE SEG ID NOS: 47374 TYPE: PRT CREATER FILE SECTION THREFACE SEG ID NOS: 47374 TYPE: PRT CREATER FILE SECTION THREFACE SEG ID NOS: 47374 TYPE: PRT CREATER FILE SECTION THREFACE SEG ID NOS: 47374	Alignment Scores: 3.93e-141 Length: 543
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Qy 1021 GATATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTAT 1080	Db 341 AspilediuGlyArgValaladiileivsAladiilediuHilliniHill	361 AspArgGluLysLeuGlnGluArgLeuAlaLysLeuAlaGlyGlyValAlaVallleArg	141 GITGGAGGIGCIACIACIAGAANGAANGAAGAAGAAGAAIGGIGAAGAGAIGCICIA 	Oy 1201 AATGCAACAACAGGTTGAAGAAGTATTGTCCCTGGTGGTGCTTGTTTGT	OY 1261 CGCTCCATTAAAGTCCTTGATGATAATAAACCTGCTGATGATGATGATGCTGCTGGACTT 1320	1321 AATATCATCGGTCGTTCTTGAAGAGCCTTTACGTCAAATTGCTGCAAATGCTGGCTAT 138	OY 1381 GAAGGTTCTATTGTAGAAAAGTTCGTGAACCAAAAGATGGTTTTGGATTTAAT 1437	Oy 1438 GCTGCATCAGAAGAATATGAAGACCTTATTAAAGCTGGTGTCATTGATCCTAAAAAAGTT 1497	QY 1498 ACACGTATTGCATTACAAATGCAGCATCAGTAGCCTTCCTT	1558 GCTATTGCTC	Oy 1615 GGTGCTATG 1623	RESULT 10 US-10-369-493-11922 ; Sequence 11922, Application US/10369493 ; Publication No. US20030233675A1	gwei Gregory Steven	; APPLICANT: Goldman, Barry S. ; APPLICANT: Chen, Xianfeng ; TITLE OP INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES	EFERENCE: 38- T APPLICATION T FILING DATE APPLICATION N	; PRIOR FILING DATE: 2002-02-21 ; NUMBER OF SEQ ID NOS: 47374 ; SEQ ID NO 11922 ; LENGTH: 542	; TYPE: PRT ; ORGANISM: Mesorhizobium loti US-10-369-493-11922	Alignment Scores: 6.3e-141 Length: 542 Pred. No.: 1826.00 Matches: 366 Percent Similarity: 82.59% Conservative: 80
Best Local Similarity: 68.88\$ Mismatches: 96 Query Match: 61.61\$ Indels: 3 DB: 3	4A-1 (1-1647) x US-10-369-493-15265 (1-543)	OY 1 ATGGCTTCTAAAGAAATCCTTTTTGATGCTGAAAAGCCTGTGAAAACTTTCACGAGGTGTA 60	Qy 61 GATAAACTTGGAAATGCTGTTAAAGTAACACTTGGACCTAAAGGCGGTAATGTCGTTATT 120	Qy 121 GAAAAGTCTTTTGGTTCCCCAGTTACAAAAGATGGTGTATCTGTTGCAAAAGAAATT 180 :::	Qy 181 GAACTTGAAGATAAGTTTGAAAATATGGGGGCTCAAATGGTTAAAGAAGTAGCTCCCAAA 240	ACTAGCGATATTGCTGGTGATGGAACTACAACAGCAACAGTCCTTGCAAAAGCTATTTAT	Oy 301 CGTGAAGGTGTAAAACTTGTAGCAGCTGGTCGTAATCCTATGGCCATTAAACGTGGCCATA 360	Oy 361 GATAAAGCTGTTGCTGATTACTAAAGAACTAAGGACATTACAAAGCCTACTCGTGAC 420	CARARAGBARIAGCTCARGITGGBACCATTTCTGCBARCTCTGATACACAATAGGTAAT ::: :::	Qy 481 ATCATAGCTGAAGCTATGGCTAAAGCTTGGAAAAGGGGGTGTTATCACAGTTGAGGAAGCT 540	Qy 541 AAAGGTCTTGAAACTACAFTAGATGTGGTTGAAGGAATGAAGTTTGACCGTGGCTACCTC 600	Qy 601 TCTCCATACTTTGTAACTAATCCTGAGAAAATGGTTTGTGGAACTTGATAACCCTTATATC 660 Db 201 SerProTyrPheValThrAsnProGluLysMetValAlaAspLeuGluAspAlaTyrIle 220	Qy 661 CTTTGTAATGAGAAAAGATTACTAGGAAGACATGCTACCAATCTTAGAACAAGTT 720	Qy 721 GCTAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCA 780 :::	QY 781 ACACTTGTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGT 840	OY 841 TTTGGTGAACGCCGTAAAGCTATGCTTGAAGATATTGCTATCCTTACTGGAGAGAAGCA 900 ::	OY 901 ATATTIGAAGAICGTGGTATAAAGCTIGAAAAGCTTGTCTTTAGGAACAGCT 960	Qy 961 AAACGTGTAGTTATTGACAAAGAAAATACTACTATCGTTGATGGTGCTGGAAAATCAGAA 1020 :::

PRODUCTION OF

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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Greyen C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION (TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR PILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                       1141 GTTGGAGCTGCTACTGAAACTGAAATGAAAGAGAAGAAGGATCGTGTAGAAGATGCTCTA 1200
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               1021 GATATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGGTCAGATTAT 1080
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                                 341 GlulleGlnGlyArgValSerGlnIleLysSerGlnIleGluGluThrThrSerAspTyr
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Sequence 15838, Application US/10369493
; Sequence 15838, Application US/10369493
; Publication No. US20030238675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: BEARESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: UMBER: US/10/369,493
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
                  GATCGTGAAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCAT 1140
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LENGTH: 540
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PRIOR FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
FEGO ID NO 12170
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. Sequence 12170, Application US/10369493

. Publication No. US20030233675A1

. GENERAL INFORMATION.
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|MetAlaAlaLysAspIleArgPheGlyGluAspAlaArgThrArgMetValArgGlyVal
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US/10/369,493
GATCGTGAAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCAT 1140
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ArgAlaLeuValAlaValGlyAsnLeuThrGlyAlaAsnGluAspGlnThrHisGlyIle 440
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Mismatches:
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Oy 1081 GATCGTGAAAACTTCAAGAACGTCTTGCCAAAACTTGTTGGTGGAGTAGCTGTTATCCAT 1140	Db 401 AshAlaThrArgAlaAlaValGluGluGluGlyTleValProGlyGlyValAlaLeuLeu 420 Qy 1261 CGCTCCATTAAAGTCCTTGATGATATTAAACCTGCTGATGATGATGATGACTTGCTGGACTT 1320	1381 GAAGGITCTATTGITGAAAAAGTITCGIGAACCAAAAGAIGGITTTGGATTTAAT 1	500 ValArgThrAlaLeuGlnAspAlaAlaGerValAlaGlyLeuLeuValThrThrGluAla 5 1558 GCTATTGCTGAAAAACCAGAACCTAAAAAAGATATGCCTATG 1 520 MetileAlaGluAlaProLysbysGluSerAlaGlyGlyGlyGlyMetProGlyGlyMet 5 1600 CCTGGCGGTGGTATGGGTGGTATGGGTGGTATGGGTGGTATGGGTGGT	RESULT 14 US-10-369-493-167 is 369-493-167 is Sequence 167, Application US/10369493 publication No. US20030233675A1 igenment 167 general incorration. APPLICANT: Cao, Vongwei APPLICANT: Slater, Steven C. APPLICANT: Goldman, Barry S. APPLICANT: Chen, Xianfeng TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B CURRENT APPLICATION NUMBER: US 60/369,493 CURRENT APPLICATION NUMBER: US 60/360,039 PRIOR PLILING DATE: 2003-02-28 PRIOR PLILING DATE: 2003-02-21 NUMBER OF SEQ ID NOS: 47374 SEQ ID NO 167 LENGTH: 545 TYPE: PRT ORGANISM: Aquifex aeolicus	Alignment Scores: 1.19e-137 Length: 545 Pred. No.: 1786.00 Matches: 352 Scorett Similarity: 82.29% Mismatches: 94 Best Local Similarity: 64.94% Mismatches: 86 Query Match: 60.18% Indels: 2 DB:
US-09-077-574A-1 (1-1647) x US-10-369-493-12170 (1-552) QY	4.1 ASPLySSerPheGlyAlaProArglleThrLySASpGlyValThrValAlaLySGluIle 4.1 AspLySSerPheGlyAlaProArglleThrLySASpGlyValThrValAlaLySGluIle 4.1 AspLySSerPheGlyAlaProArglleThrLySASpGlyValThrValAlaBerLyS 4.1 ACTAGCGATATTGTGTGTAAAATATGGGACCTCAAACAGCAACAGCACAGTCCTTGCAAAGCTATTTAT 4.1 ACTAGCGATATTGCTGGACTGGAACTACAACAGCGAACAGTCCTTGCACAAGCTATTTAT 4.1 ACTAGCGATATTGCTGGAACTACAACAGCAACAGTCCTTGCACAAGCTATTTAT 4.1 ACTAGCGATATTGCTGGAACTACAACAGCAACAGTCCTTGCACAAGCTATTTAT 4.1 ACTAGCGATATTTAT 4.1 ACTAGCGATATTATTATTATTATTATTATTATTATTATTATTATTA	DD 81 ThrasnaspilahadiyaspdiyThrThrThrahaThrvalLeuahadinserileval 100 301 CGTGAAGGTGTAAAACTTGTAGCAGCTGGTGAATCCTATGGCCATTAAACGTGGCATA 360 :::	421 CAAAAGAAATAGCTCAAGTTGGAACCATTTCTGCAAACTACAACAATAGGTAAT 480 141 SerGluGluValAlaGlnValGlyThrIleAlaGlyAsnGlyAspGluSerValGlyLys 160 481 ATCATAGCTGAAGCTAATGGCTAAAGTTGGAAAAGGGGGTGTTATCACAGTTGAGGAAGCT 540 591 MetileAlaGluAlaMetGlnLySValGlyAsnGluGlyValIleThrValGluGluAla 180 90 541 AAAGGTCTTGAAACTACATTAGATGAAGAATGAAGGTTGAAGGTTACCCGGGCTACCTC 600 181 LANSTDAAAGTACATTAGATGAAGTGAAAGAATGAAGGTTGAAGGTTACCGTGGCTACCTC 600 181 LANSTDAAAGTACATTAGATGAAGTGAAAGAATGAAGTTTGAACGTGGGCTACCTC 600 181 LANSTDAAAGTACTAGAATGAAGTGAAAGAAAGATTAGAACGTTGAAGGTTACAAGTATAGAATGAAAGAATACAATAGAAATAGAAAAAGTATAGAAAAAGTATAGAAAAAAA	601 TCTCCATACTTGTAACTAATCCTGAGAAATGGGTTGGAGAACTTGATAACCCTTATATC [Db 301

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APPLICANT: Gao, Yongwei
APPLICANT: Glarer, Steven C.
APPLICANT: Glater, Steven C.
APPLICANT: Glater, Staven C.
APPLICANT: Glater, Staven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TILLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION (TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TILLE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US 10/10/369, 493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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Perfect score:

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Searched:

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APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
CORRESPONDENCES: 44
CORRESPONDENCE ADDRESS:
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                                                          US-08-466-248-33

US-08-466-248-33

US-08-466-248-33

US-08-468-041-2

US-09-468-041-2

US-09-198-452A-153

US-08-472-697-30

US-08-432-697-30

US-08-432-697-30

US-09-613-303-1

US-09-97-080-160

US-09-97-080-160

US-09-324-542-160

US-09-613-303-4

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US-08-447-154-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILLOATION NUMBER: US/08/467,822 FILING DATE: 06-JUN-1995
             US-08-256-847C-7
US-08-467-822-33
US-08-432-697-33
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APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MX-1995
CLASSIFICATION: 435
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5843460
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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ADDRESSEE:
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-Q=/Cgn2_1/USPTO_spool_p/USO9077574/runat_28012004_125847_11658/app_query.fasta_1.1799
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-Q=/Cgn2_1/USPTO_spool_p/USO8010-1-MATRIX=blosum62_-TRANS=human40.cdi
-LOOPEXT=0 -UNITS=bits -START=1 - END=1 - MATRIX=blosum62_-TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 - THR SCORE=pct - THR MAX=100 - THR MIN=0 - ALIGN=15
-MODB=LOCAL_OUTPRT=ptc - NORM=ext - HEAPSIZE=500 - MINLEN=0 - MAXLEN=200000000
-NORS=LOCAL_OUTPRT=ptc - NORM=ext - HEAPSIZE=500 - MINLEN=0 - MAXLEN=200000000
-NORS=LOCAL_OUTPRT=ptc - NORM=ext - HEAPSIZE=500 - MINLEN=0 - LONGCLOG
-NORS=LOCAL_OUTPRT=ptc - NORM=ext - HEAPSIZE=100 - LONGCLOG
-NORS=LOCAL_OUTPRT=ptc - NORM=0 - WAIT - DSEBLOCK=100 - LONGCLOG
-DEV_TIMBOUT=120 - WARN_TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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Sequence 32, Appl
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-432-697-31
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US-08-467-822-32
US-08-467-822-32
US-08-466-660-6
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                                                                                                                                                                                                                            262 ValValAsnAsnMetArgGlyIleValLysValCysAlaValLysAlaProGlyPheGly
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667 AATGAGAAAAAGATTACTAGCATGAAAGACATGTACCAATCTTAGAACAAGTTGCTAAA
                   SerGlyArgProLeuLeuIlelleAlaGluAspIleGluGluGluGluAlaLeuAlaThrLeu
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Mismatches:
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                                                                                                             03495.0137-02000
                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAX-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
                                                                     NAME: Meyers, Kenneth J.
REGISTRATION WUMBER: 25,146
REFRENCE/DOCKET NUMBER: 03495
TELECOMUNICATION INPORMATION:
TELEPHONE: (202) 408-4400
INPORMATION FOR SEQ ID NO: 5EQUENCE CHARACTERISTICS: 31:
                                                                                                                                                                                                                                                                                                                                                 5.71e-170
1844.00
82.02%
67.16%
62.13%
                                                                                                                                                                                                                LENGTH: 548 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-08-467-822-31
                                                                                                                                                                                                                                                                  linear
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                  TOPOLOGY:
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342 AsnalaArgileAlaGlnIleArgAlaGlnMetGluGluThrThrSerAspTyrAspArg 361
                                                                                                                                              427 GAAATAGCTCAAGTTGGAACCATTTCTGCAAACTCTGATACAACAATAGGTAATATCATA
                                                                                                                                                                                              GCTGAAGCTATGGCTAAAGTTGGAAAAGGAGGTGTTATCACAGTTGAGGAAGCTAAAAGGT
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|82 LeuGluAsnGluLeuTyrValValGluGlyMetGlnPheAspArgGlyTyrIleSerPro
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                                                     367 GCTGTTGTTGCTGTTACTAAAGAACTAAGCGACATTACAAAAGCCTACTCGTGACCAAAAA
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         APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INPECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
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| AlaLysGluLeuArgPheGlyAspAspAlaArgLeuGlnMetLeuAlaGlyValAsnAla
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|SerTyrGlyAlaProThrValThrLysAspGlyValSerValAlaLysGlulleGluPhe
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                                                                                                                                                                   ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,697
FILING DATE: 02-MAY-1995
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
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                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                   STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 408-4000 TELEPAX: (202) 408-4400 INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS:
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1844.00
82.02%
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MEDIUM TYPE: Floppy disk
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                                                                                                                                NUMBER OF SEQUENCES: 4.
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       APPLICANT:
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                                           Conservative:
Mismatches:
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           Length:
Matches:
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                                             Percent Similarity:
Best Local Similarity:
Alignment Scores:
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                                                                                Query Match:
                Pred. No.:
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APPLICANT: Sauchbaum, Sebastien
APPLICANT: Sauchbaum, Sebastien
APPLICANT: Ferrero, Stichard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
CORRESPONDENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                              GAAAAACCAGAACCTAAAAAAAATATGCCTATGCCTGGCGTGGTATGGGTGTATGGGT 1626
                                                                                                 GCATTACAAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGCGCTATTGCT 1566
                                 GGAGAATATGAAGACCTTATTAAAGCTGGTGTCATTGATCCTAAAAAAGTTACACGTATT 1506
                                                                                                                                                                                  521
   SerValValValAsnLysValAlaGluHisLysAspAsnTyrGlyPheAsnAlaAlaThr 481
                                                     ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/466,248
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
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                                                                                                                                                                                                                                                                                                                          Sequence 31, Application US/08466248
Patent No. 6258359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 1627 GGTATGGACGGTATG 1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (202) 408-4000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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CITY: Washington
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546 181 909

Score: 1820.50 Matches: 366 Percent Similarity: 80.33% Conservative: 75 Best Local Similarity: 66.67% Mismatches: 103 Query Match: 61.34% Indels: 5 DB: 4 Gaps: 2 US-09-077-574A-1 (1-1647) x US-09-252-991A-24209 (1-551) Oy 1 ATGGCTTCTAAAGAATCCTTTTGATGCTAAAAGCCCGTGAAAAACTTTCACGAGGTGTA 60	Oy 61 GATAAACTTGCAAATGCTGTTAAAGTAACACTTGGACCTAAAGGCGGTAATGTCGTTATT 120 ::: :::		Oy 301 CGTGAAGGTGTAAAACTTGTAGCAGGTCGTAATCCTATGGCCATTAAACGTGGCATA 360 105 AsnGluGlyLeuLysAlaValAlaAlaGlyMetAsnProMetAspLeuLysArgGlyIle 124 Qy 361 GATAAAGCTGTTGTTGCTGTTACTAAAGAACTAAGGACATTACAAAGCCTACTCGTGAC 420 105 ASTAAAGCTGTTATTGTTGTTGTTGTTAAAAGAACTAAAAAAGCGAACTAACAAAAGCGTAATAAAAAAAA	421 CAAAAGAAATAGCTCAAGTTGGAACCATTTCTGCAAACTGTGATACAATAGGTAAT	Oy 481 ATCATAGCTGAAGCTATGGCTAAAGTTGGAAAAGGAGGTGTTATCACAGTTGAGGAAGCT 540	Qy 601 TCTCCATACTTTGTAACTAATCCTGAGAAAATGGTTTGTGAACTTGATAATC 660	OY 721 GCTAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCA 780	265 ThrLeuvalvalhanAsmAsmAsmGlyIlevalLysvalAlaAlaValLysAlaProGly 841 TTTGGTGAACGCCGTAAAGCTATGAAGATATTGCTATCCTTACTGGAGGAGGAGCA 285 Phell:::	203 FIECTYABPATGATGTATAAAGCTTGAAAATGTAAGCTTGTCTTTAGGAACAGCT 901 ATATTTGAAGATCGTGGTATAAAGCTTGAAAATGTAAGCTTGTCTTTAGGAACAGCT 1	COT TANKS OF CANALIST LONG THE LONG THE COLL COLL COLL COLL CANALIST CANALI
967 GTAGTTATTGACAAAGAAAATACTATCGTTGATGGTGCTGGAAAATCAGAAGATATT 1	362 . 1147 382 1207	4 4 4 4	1387 TCTATTGTTGTAGAAAAGTTCGTGAACGAAAGATGTTTTGGATTTAATGCTGCATCATCATCATCATCATCATCATCATCATCATCATCATC	Db 482 GlyGluTyrGlyAspMetValGluMetGlyIleLeuAspProThrLysValThrArgMet 501 Qy 1507 GCATTACAAAATGCAGCATCAGTAGCCTCCTTACTTCTACAGAAGGGCTATTGCT 1566	1567 GAAAAACCAGAACCITAAAAAGATATGCCTATGCCTGGCGGGGGTGGTAGGTGGTGGTTGGGT 1	544 US/09252991A ield et al.	; TITLE OF INVENTION: ACCIDIT AND ACTION ACID SECTION OF PROPERTY. ; TITLE OF INVENTION: ARCHGINGSA FOR DIAGNOSTICS AND THERAPEUTICS. ; FILE REFERENCE: 107196.136 (10.0/09/252,991A); CURRENT APPLICATION NUMBER: 1089-02-18 ; CURRENT FILING DATE: 1999-02-18 ; PRIOR APPLICATION NUMBER: US 60/074,788	; PRIOR FILING DATE: 1998-02-18 ; PRIOR APPLICATION NUMBER: US 60/094,190 ; PRIOR FILING DATE: 1998-07-27 ; NUMBER OF SEQ ID NOS: 33142 ; LENGTH: 551		

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961 AAACGTGTAGTTATTGACAAAGAAATACTACTATCGTTGATGGTGCTGGAAAATCAGAA 1020
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|LeuLeuValAspLysIleSerAsnIleArgGluLeuIleSerValLeuGluAlaVal
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                                                                                        GATAAACTTGCAAATGCTGTTAAAGTAACACTTGGACCTAAAAGGCCGTAATGTCGTTATT
                           ATGGCTTCTAAAGAAATCCTTTTTGATGCTAAAAGCCCGTGAAAAACTTTCACGAGGTGTA
                                                           7 MetSerAlaLysAspValLysPheGlyAspSerAlaArgSerLysMetIleAlaGlyVal
US-09-077-574A-1 (1-1647) x US-09-328-352-5508 (1-550)
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPBUTICS
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPBUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5508
LENGTH: 550
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                                                 GATATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTAT 1080
                                                                                                             GATCGTGAAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCAT 1140
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                                                                 445 AlaLeuLeuArgArgAlaValGluSerProLeuArgGlnIleValAlaAsnAlaGlyAsp
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| 525 ValAlaGluIleValGlu------AspLysProAlaMetGlyGlyMetProAspMet
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Patent No. 6562958
GENERAL INFORMATION:
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US-09-328-352-5508
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Best Local Similarity:
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GAICGIGAAAAACTICAAGAACGICTIGCAAAACTIGIIGGIGGAGIAGCIGITAICCAI 1140
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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FILING DATE: 06-JUN-1995
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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Conservative:
Mismatches:
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                                                                                                                                                                                                                       NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (202) 408-4000
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58.66%
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APPLICATION NUMBER: US 00
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
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NAME: Meyers, Kenneth J.
                            19-MAY-1995
                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
FILING DATE: 19-MAY
CLASSIFICATION: 435
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481 AlaThrGluGluTyrGlyAsnMetIleAspMetGlyIleLeuAspProThrLysValThr
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              GCTAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCA
                                                                                                                                                          ThralaValValValAsnThrIleArgGlyIleValLysValAlaAlaAlaValLysAlaProGly
                                                                                                                                                                                                                                         ATATITIGAAGATCGTGGTATAAAGCTTGAAAATGTAAGCTTGTCTTCTTTAGGAACAGCT
                                               CTTTGTAATGAGAAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTT
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Sequence 3, Application US/09472971

Patent No. 6197947

GENERAL INFORMATION:
APPLICANT: SOGO, KAJOV
APPLICANT: YANGI, Hideki
CURRENT FINJENDE INVENTION: TRIGGER FACTOR EXPRESSION PLASMIDS
FILE REFERENCE: 1422-409P
CURRENT APPLICATION NUMBER: US/09/472,971
CURRENT FILING DATE: 1999-12-28
GARLIER APPLICATION NUMBER: JP10-372965
FARLIER FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 7
SOGTWARE: PATENTIN Ver. 2.1
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Mismatches:
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201 SerProTyrPheIleAsnLysProGluThrGlyAlaValGluLeuGluSerProPheIle 220
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                                                                                                                                                                       AAACGTGTAGTTATTGACAAAGAAAATACTACTATCGTTGATGGTGCTGGAAAATCAGAA
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521 ValThrAspLeu-----ProLysAsnAspAlaAlaAspLeuGlyAlaAlaGlyGlyMet
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                                                                                         GCTAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTGAAGGTGAAGCACTTGCA
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                                               .021 GATATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTAT
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                            CTTTGTAATGAGAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTT
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; Sequence 32, Application US/08432697
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GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Thereo, Richard L.
APPLICANT: Thiberey, Jean-Michel
TITLE OF INVENTION: IMMINGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: COMPOSITIONS, AND NUCLBIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYBEPTIDES
NUMBER OF SEQUENCES: 44
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                                                                                                                                                                                                                 Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/432,697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-077-574A-1 (1-1647) x US-08-432-697-32 (1-548)
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REFERENCE/DOCKET NUMBER: 03495.0137-00000
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMBER: US/08/432,697
02-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                        1300 I Street, N.W.
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INFORMATION FOR SEQ ID NO: 32:
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                                                                                                                                                                                                                                                                                           STATE: D.C.
CONNTRY: USA
ZIP: 20005-3315
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
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58.66%
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Best Local Similarity:
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TOPOLOGY: lin
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                                                                                                                                                                                                                                        ADDRESSEE:
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MOLECULE TYPE: protein
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US-08-466-248-32
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CGTGAAGGTGTAAAACTTGTAGCAGCTGGTCGTAATCCTATGGCCATTAAACGTGGCATA
                                                           GATAAAGCTGTTGTTGCTGTTACTAAAGAACTAAGCGACATTACAAAGCCTACTCGTGAC
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|LeuLeuAlaAspLysLysIleSerAsnIleArgGluMetLeuProValLeuGluAlaVal
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GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
1381 GAAGGTTCTAFTGTTGTAGAAAAGTTCGTGAACCAAAAGATGGTTTTGGATTTAATGCT 1440
                                                                                                                                                                                                                         1501 CGTATTGCATTACAAATGCAGCATCAGTAGCCTCCTTACTACTACAGAATGCGCT 1560
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                                   ValThrAspLeu-----ProLysAsnAspAlaAlaAspLeuGlyAlaAlaGlyGlyMet
                                                                                                          1441 GCATCAGGAGAATATGAAGACCTTATTAAAGCTGGTGTCATTGATCCTAAAAAAGTTACA
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481 AlaThrGluGluTyrGlyAsnMetIleAspMetGlyIleLeuAspProThrLysValThr
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CARRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,248
FILING DATE: 06-JUN-1995
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FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 32, Application US/08466248 Patent No. 6258359
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TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 32
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REGISTRATION NUMBER: 25
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1201 AATGCAACAAGAGCTGCGGTTGAAGAAGGTATTGTCCCTGGTGGTGGTACTGCTTTTGTC 1260
                                                                                                                                                GATCGTGAAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCAT 1140
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    CGTATTGCATTACAAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGCGCT 1560
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PAPLICANT: Rappuoli, Kino
TITLE OF INVENTION: Helicobacter
TITLE OF INVENTION: for Vaccines
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Patent No. 6077706
GENERAL INFORMATION:
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APPLICANT: Bugnoli, Massimo
APPLICANT: Telford, John
APPLICANT: Macchia, Giovanni
APPLICANT: Rappuoli, Rino
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Chiron Co.
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US-08-470-260-6
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353
118
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                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                             US-09-077-574A-1 (1-1647) x US-08-466-248-32 (1-548)
                                    5.37e-160
1741.00
77.78%
64.30%
58.66%
                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                         Alignment Scores:
US-08-466-248-32
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| AlaAlaGluAlaIleIleAsnGluLeuLysLysAlaSerLysLysValGlyGlyLysGlu 141
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350
73
120
3
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                              FILING DAIR:
CLASSIBFCATION:
PRIOR APPLICATION NUMBER: US 08/256,848
PRIOR APPLICATION NUMBER: US 08/256,848
FILING DATE: 21-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNG, BARDAR G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0316.001
TELEPHONE: (510) 601-2708
TELEPHONE: (510) 601-2708
TELEPHONE: (510) 655-3542
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
TRANSTH: 546 amino acids
                                                    US/08/470,260
                                                                                                                                                                                                                                                                                                                                           2.65e-158
1723.50
77.47%
64.10%
58.07%
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MOLECULE TYPE: protein
US-08-470-260-6
                                                 APPLICATION NUMBER:
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                        667 AATGAGAAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTTGCTAAA
GTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCAACACTT
                                                                                                                                                                                                                                                                         GTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGTTTTGGT
                                                                     TACTTTGTAACTAATCCTGAGAAAATGGTTTGTGAACTTGATAACCCTTATATCCTTTGT
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GTAGTTATTGACAAAGAAAATACTACTATCGTTGATGGTGCTGGAAAAATCAGAAGATATT 1026
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LysAspArgValAlaGlnIleLysThrGlnIleAlaSerThrThrSerAspTyrAspLys 361
    182 IleGluAspGluLeuAspValValGluGlyMetGlnPheAspArgGlyTyrLeuSerPro 201
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                                                                                                                                                                          GluGlyLysProLeuLeullelleAlaGluAspIleGluGlyGluAlaLeuThrThrLeu
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                                                                                            667 AATGAGAAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTTGCTAAA
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APPLICANT: Covacci, Antonello
APPLICANT: Bugnoli, Massimo
APPLICANT: Bugnoli, Massimo
APPLICANT: Rapuoli, Giovanni
APPLICANT: Rapuoli, Rino
TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And
TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And
TITLE OF INVENTION: Diagnostics
FILE REFERENCE: CHIRO044
CURRENT APPLICATION NUMBER: US/08/471,491B
CURRENT FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
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                                                           Sequence 6, Application US/08471491B Patent No. 6090611
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US-08-471-491-6
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TYPE: PRT
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ORGANISM: Helicobacter pylori
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                                                 APPLICANT: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
APPLICANT: Costantino, Paolo
APPLICANT: Costantino, Paolo
TITLE OF INVENTION: Conjugates Formed From Heat Shock Proteins And Oligo or Polysacch
FILE REFERENCE: CHIR-0042
CURRENT APPLICATION NUMBER: US/08/256,847C
CURRENT APPLICATION NUMBER: PCT/EP93/00516
PRIOR FILING DATE: 1994-11-01
PRIOR PPLICATION NUMBER: F192A000058
PRIOR PPLICATION NUMBER: F192A000058
PRIOR FILING DATE: 1992-03-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
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     Sequence 1, Application US/08256847C Patent No. 6403099
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Rostantino, Paolo
APPLICANT: Costantino, Paolo
APPLICANT: No. 6403099e111, Francesco
TITLE OF INVENTION: Conjugates Formed From Heat Shock Proteins And Oligo or Polysacch
FILE REFERENCE: CHIR-0042
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|SerTyrGlyAlaProSerIleThrLysAspGlyValSerValAlaLysGluIleGluLeu
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Matches:
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                                                                                                                                CURRENT PELICATION NUMBER: US/08/256,847C
CURRENT FILING DATE: 1994-11-01
PRIOR APPLICATION NUMBER: PCT/BE93/00516
PRIOR FILING DATE: 1993-03-08
PRIOR FILING DATE: 1993-03-08
PRIOR FILING DATE: 1992-03-06
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 7
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
Gaps:
               Sequence 7, Application US/08256847C Patent No. 6403099
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1723.50
77.47%
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; ORGANISM: H. pylori
US-08-256-847C-7
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                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
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       US-08-256-847C-7
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APPLICANT: Sauerbaum, Sebastien
APPLICANT: Berrero, Richard L.
APPLICANT: Thiberge, Jaan-Michard L.
APPLICANT: Thiberge, Jaan-Michard L.
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS ACAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES
NUMBER OF SEQUENCES: 44
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ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/447,177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/467,822
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                         Sequence 33, Application US/08467822
Patent No. 5843460
                                                                                                                                                                                                                                                                                       1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
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1721.00
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64,768
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CLASSIFICATION: 435
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                             GENERAL INFORMATION:
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CLASSIFICATION:
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SUMMARIES
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Copyright (c) 1993 - 2004 Compugen Ltd
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The GroEL heat shock protein (AAW16678) of Lawsonia intracellularis can be used in vaccines to protect birds and animals against intestinal diseases, esp. to protect pigs against porcine problet the continuation of continuatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccine for treating or preventing Lawsonia intracellularis infection - especially in pigs, containing non-pathogenic form of bacterium or its components
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 38-42; 94pp; English.
                                     96WO-AU00767.
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95AU-0006910
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(PIGR-) PIG RES & DEV CORP.
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                                                                                                              22 LeuAlaAspAlaValLysValThrLeuGlyProLysGlyArgAsnValValLeuGluLys
                                                                                                                                                                                                                                                                                          62 GluAspLySPheGluAsnMetGlyAlaGlnLeuValLysGluValAlaSerLySThrAsn
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222 ThrAspLysIysIleSerAsnIleGlnAspLeuLeuProValLeuGluGluValAlaGln
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TCTAAAGAAATCCTTTTTGATGCTAAAGCCCGTGAAAAACTTTCACGAGGTGTAGATAAA
                                       2 AlaLysAspIleLysPheGlyGluGluAlaArgArgArgAlaMetLeuArgGlyValAsnAla
                                                                                       CTTGCAAATGCTGTTAAAGTAACACTTGGACCTAAAGGCCGTAATGTCGTTATTGAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    describes Streptococcal Haps, designated Hap60. These proteins, their fragments, variants and fusion proteins, are used to elicit or enhance an immune response against Streptococcus, and to elicit a similar response to a target antigen fused to the protein. Unlike other immunological carriers, Hap60 proteins are not immunosuppressive so immunological carriers, Hap60 proteins are not immunosuppressive so provide an increased response to any conjugated or fused antigen. Also, where used for cancer control, they lack the side effects associated with endotoxins. They can also be used to detect specific antibodies and in treatment or prevention of tumours (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or liver). The Hap60 polynucleotide is used for recombinant production of the protein, as a source of primers and probes for detecting streptococci in standard hybridization/amplification assays, and therapeutically in gene
                                                                                         540
    501 ArgileAlaLeuGlnAsnAlaAlaSerValAlaSerLeuLeuLeuThrThrGluCysAla 520
                                                                         521 IleAlaGluLySProGluProLySLySASpMetProMetProGlyGlyGlyMetGlyGly
                                                1561 ATTGCTGAAAAACCAGAACCTAAAAAAGATATGCCTATGCCTGGCGGTGGTATGGGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heat shock protein; Hsp; immune response; immunological carrier;
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Query Match:
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1087 GAAAAACTICAAGAACGICITIGCAAAACITGITGGIGGAGIAGCIGITAICCAIGITGGA 1146

341 AlaGlyArgValAlaGinileArgSerGinileGiuGiuSerThrSerAspTyrAspLys 360

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Gaps:

JS-09-077-574A-1 (1-1647) x AAY23930 (1-545)

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1267 ATTAAAGTCCTTGATGATATTAAACCTGCTGATGATGATGAACTTGCTGGACTTAATATC 1326
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ValleuArgAlaLeuGluAlaProLeuArgGlnIleAlaGluAsnAlaGlyLeuGluGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; Hsp; immune response; immunological carrier;
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Disclosure; Fig 10A-E; 176pp; English

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AAV23905-30 represent heat shock proteins (Hsps). The specification describes Streptococcal Hsps, designated Hsps0. These proteins, their fragments, variants and fusion proteins, are used to elicit or enhance an immune response against Streptococcus, and to elicit a similar response to a target antigen fused to the protein. Unlike other immunological carriers, Hsp60 proteins are not immunosuppressive so provide an increased response to any conjugated or fused antigen. Also, where used for cancer control, they lack the side effects associated with endotoxins. They can also be used to detect specific antibodies and in treatment or prevention of tunours (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or liver). The Hsp60 protein, as pource of primers and probes for detecting streptococci in standard hybridization/amplification assays, and therapeutically in gene
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chitinase; groEL; chiA; antigen; vaccine;

protein sequence

Pseudomonas aeruginosa groEL

(first entry)

L8-APR-2001

detection; infection; immune response.

aeruginosa;

Pseudomonas

diagnosis;

Pseudomonas aeruginosa

WO200102577-A1

11-JAN-2001

03-JUL-2000; 2000WO-GB02554

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                 907 GAAGATCGTGGTATAAAGCTTGAAAATGTAAGCTTGTCTTCTTTAGGAACAGCTAAACGT
 AATGAGAAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTTGCTAAA
                                                                                                                                      262 ValValAsnAsnMetArgGlyIleValLysValCysAlaValLysAlaProGlyPheGly
                                                      GTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCAACACTT
                                                                                                             GTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAAGCTCCTGGTTTTGGT
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AAB69060 standard; Protein; 547 AA.

AAB69060;

AAB69060 ID AAB6 XX AC AAB6

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                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes antigenic Pseudomonas aeruginosa proteins (P1). The P. aeruginosa proteins have antibacterial activity and can be used in vaccines and as antagonists. The proteins or their fragments, or antibodies are useful in the detection and/or diagnosis of P. aeruginosa. They are also useful for producing a vaccine and inducing an immune response against P. aeruginosa infection. An agent capable of antagonising, inhibiting or otherwise interfering with the function or expression of Pl are useful in the manufacture of a madicament for the treatment or prophylaxis of P. aeruginosa infections. The present sequence represents a specifically claimed P. aeruginosa großi protein sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                            Antigenic Pseudomonas aeruginosa proteins, useful in the detection and/or diagnosis of P. aeruginosa infections and for producing vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATAAACTTGCAAATGCTGTTAAAGTAACACTTGGACCTAAAAGGCCGTAATGTCGTTATT
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                                                                                                                                                                                                                                                                         Wilkinson
                                                                                                                                                                                                                                                                           Sizer PJH,
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1381 GAAGGTTCTATTGTTGTAGAAAAGGTTCGTGAACCAAAAGATGGTTTTGGATTTAATGCT 461 GlubroServalValValAspLysValLysGlnGlySerGlyAsnTyrClyPheAsnAla 1441 GCATCAGGAGAATATGAAGACCTTATTAAAGCTGGTGTCATTGATCCTAAAAAAGTTACA	Oy 1561 ATTGCTGAAAACCTAAAAAATTGCTATGCTGCGGTGCTATG 1614 Db 521 ValAlaGluIleValGluApLysPrOAlaMetGlyGlyMetProAspMet 537 Oy 1615 GGTGGTATGGGTGGTATGGGCGTATG 1641 Db 538 GlyGlyMetGlyGlyMetGlyGlyMet 546 RESULT 5 AAR67381 standard; Protein; 547 AA.	AC AAR67381; XX XX DT 25-MAR-2003 (updated) DT 22-JUN-1995 (first entry) XX XX DE L. pneumophila HtpB gene product. XX	OS Legionella pneumophila. XX	XX XX PA (INSP) INST NAT SANTE & RECH MEDICALE. PA (INSP) INST PASTEUR. XX	develop prods. for detection, treatment and prevention of Helicobacter infection. Disclosure; Fig. 7A(i-vii); 168pp; English. The sequence of the Helicobacter pylori heat shock protein (given in AAR67374) was compared to that of other GroEL-lik proteins from Legionella pneumophila (AAR67381), Escherichi (AAR67382), Chlamydia psittaci (AAR67383), Mycobacterium le (AAR67382) and human mitochondrial protein Pl (AAR67385), a of homology were identified. (Updated on 25-MAR-2003 to correct PN field.)	XX XX Sequence 547 AA; Alignment Scores: Pred. No.: Coore: Score: Percent Similarity: 81.65% Conservative: 82
81 AlaAsnAspAlaAlaGlyAspGlyThrThrThrAlaThrValLeuAlaGlnAlaIleVal 100 301 CGTGAAGGTGTAAACTTGTAGCAGCTGGTCGTAATCCTATGGCCATTAAACGTGGCATA 360 101 AsnGluGlyLeuLysAlaValAlaAlaGlyMetAsnProMetAspLeuLysArgGlyIle 120 361 GATAAAGCTGTTGTTGTTACTAAAGAACTAAGGCACATTACAAAGCCTACTCGTGAC 420 11 AspLySAlaThrValAlaIleValAlaGlnLeuLySGluLeuAlaLySProCysAlaAsp 140 421 CAAAAAGAAATAGCTCAAGTTGGAACCATTTCTGCAAACTTGGTAACAAAACAATAGGTAAT 480 11 ThrLySAlaIleAlaGlnValGlyThrIleSerAlaAsnSerAspGluSerIleGlyGln 160	481 ATCATAGCTGAAGCTATGGCTAAAGTTGGAAAAGGGGCTGTTATCACAGTTGAGGAAGCT 540 [661 CTITGTAATGAGAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTT 720		961 AAACGTGTAGTTATTGACAAAAAAAACTACTATCGTTGATGGTGCTGGAAAATCAGAA 1020	GATCGTGAAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCAT	1201 COLLOCALIMANGICIIGANGAIAITANACIGELGAIGAIGAIGAIGAIGAIGAIGAIGAIGAIT 1320 421 ArgalaLeuGlnalaileGluGlyLeuLyBGlyAspAsnGluGluGluGlnAsnValGlyIle 440 1321 AATATCATCCGTTCTTGAAGAGCCTTTACGTCAAATTGCTGCAAATGCTGGCTAT 1380 441 AlaLeuLeuArgAlalaValGluSerProLeuArgGlnIleValAlaAsnAlaGlyAsp 460

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Jocal Similarity: 66.61% Match: 16.34%	-077-574A-1 (1-1647) x ARK67381 (1-547) 7 TCTAAAGAAATCCTTTTTGATGCTAAAGCCCGTGAAAAACTTTCACGAGGTGTAGATAAA 66 7 TCTAAAGAAATCCTTTTTGATGCTAAAGCCCGTGAAAAACTTTCACGAGGTGTAGATAAA 66 8::: ::: ::: :::	67 CTTGCAAATGCTGTTAAAGTAACACTTGGACCTAAAGGCCGTAATGTCGTTATTGAAAAG 126 :::	127 TCTTTTGGTTCCCCAGTTATTACAAAAGATGGTGTATCTGTTGCAAAAGAAATTGAACTT 186 ::: ::: :::	187 GAAGATAAGTITGAAAATATGGGCGCCTCAAATGGTTAAAGAAGTAGCTCCCCAAAACTAGC 246 :::	247 GATATTGCTGGTGATGGAACTACAACAGCAACAGTCCTTGCACAAGCTATTTATCGTGAA 306 	307 GGTGTAAAACTTGTAGCAGCTGGTGGTGGTATCCTATGGCCATTAAACGTGGCATAGATAAA 366 	367 GCTGTTGTTGCTGATAACAACTAAGGGACATTACAAAGCCTACTCGTGACCAAAA 426 ::	427 GAAATAGCTCAAGTTGGAACCATTTCTGCAAACTCTGATACAACAATAGGTAATATCATA 486	487 GCTGAAGCTATGGCTAAAGTTGGAAAAGGGGTGTTATGACGTTGAGGAAGCTAAAGGT 546	547 CTTGAAACTACATTAGATGTGGTTGAAGGAATGAAGTTTGACCGTGGCTACCTCTCCA 606 	607 TACTITGTAACTAATCCTGAGAAAATGGTITGTGAACTTGATAACCCTTATATCCTTTGT 666	667 AAIGAGAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTTGCTAAA 726 :::	727 GTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGGCTTGCAACACTT 786 [787 GTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGTTTTGGT 846	847 GAACGCCGTAAAGCTAGGTTGAAGATATTGCTATCCTTACTGGAGGAAGGA	907 GAAGATCGTGGTATAAAGCTTGAAAATGTAAGCTTGTCTTCTTTAGGAACAGCTAAACGT 966 907 GAAGATCGTGGTATAAAGCTTGAAAATGTAAGCTTGTTTTAGGAACAGCTAAACGT 966 302 GluGluIleGlyLysSerLeuGluGlyAlaThrLeuGluAspLeuGlySerAlaLysArg 321	967 GTAGTTATTGACAAAAATACTACTGTTGATGGTGCTGGAAAATCAGAAGATATT 1026 :::::::::
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1267 ATTAAAGTCCTTGATGATATTAAACCTGCTGATGATGAACTTGCTGGACTTAATATC 1326
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1027 AAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTATGATCGT 1086
                                                                                                                                                                 1147 GCTGCTACTGAAACTGAAATGAAAGAGAAGAAGATCGTGTAGAAGATGCTCTAAATGCA 1206
                                                                                                                                                                                                                                              1207 ACAAGAGCIGCGGIIGAAGAAGAIATIGICCCIGGIGGIGGIACTGCIITITGICCGCICC 1266
                                                                                                                                                                                                                                                                                                                                                                                                                  1327 ATCCGTCGTTCTTTTAAGAGCCTTTACGTCAAATTGCTGCAAATGCTGGCTATGAAGGT 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1387 TCTATTGTTGTAGAAAAGTTCGTGAACCAAAAGATGGTTTTGGATTTAATGCTGCATCA 1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1447 GGAGAATATGAAGACCTTATTAAAGCTGGTGTCATTGATCCTAAAAAAGTTACACGTATT 1506
                                                                                 1087 GAAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCATGTTGGA 1146
                                                                                                                                                                                                                                                                                                                                                        Smith CJ, Thompson SE, Smith MW, Peek K, Sizer PJH, Wilkinson MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa, chitinase, groEL, chiA, antigen, vaccine, diagnosis, detection; infection; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TrcHisB expression vector großL fusion protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              061
AAB69061 standard; Protein; 574 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PROV-) PROVALIS UK LTD.
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2001-080988/09 N-PSDB; AAF32453

the detection producing vaccines Antigenic Pseudomonas aeruginosa proteins, useful in and/or diagnosis of P. aeruginosa infections and for against P. aeruginosa -

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Claim 3; Fig 26; 129pp; English.

The present invention describes antigenic Pseudomonas aeruginosa proteins (P1). The P. aeruginosa proteins have antibacterial activity and can be used in vaccines and as antagonists. The proteins or their fragments, or antibodies are useful in the detection and/or diagnosis of P. aeruginosa. They are also useful for producing a vaccine and inducing an immune response against P. aeruginosa infection. An agent capable of antagonising, inhibiting or otherwise interfering with the function or expression of P1 are useful in the manufacture of a medicament for the treament or prophylaxis of P. aeruginosa infections. The present sequence represents a specifically claimed pTrcHisB expression vector großL fusion protein sequence from the present invention

574 AA; Sequence

574 365 75 Conservative: Mismatches: Indels: Length: Matches: 1.57e-155 1819.00 80.44% 66.73% 61.29% Best Local Similarity: Query Match: Percent Similarity: Alignment Scores: .. oN

(1-574)US-09-077-574A-1 (1-1647) x AAB69061

150 900 120 240 420 ThriysAlalleAlaGlnValGlyThrileSerAlaAsnSerAspGluSerileGlyGln 190 230 GAAAAGTCTTTTGGTTCCCCAGTTATTACAAAAGATGGTGTATCTGTTGCAAAAAAATT 180 ACTAGCGATATTGCTGGTGATGGAACTACAACAGCAACAGTCCTTGCACAAGCTATTTAT 300 CGTGAAGGTGTAAAACTTGTAGCAGCTGGTCGTAATCCTATGGCCATTAAACGTGGCATA 360 CAAAAAGAAATAGCTCAAGTTGGAACCATTTCTGCAAACTCTGATACAACAATAGGTAAT 480 20 51 AsnValLeuAlaAspAlaValLysAlaThrLeuGlyProLysGlyArgAsnValValLeu 70 GAACTTGAAGATAAGTTTGAAAATATGGGCGCTCAAATGGTTAAAGAAGTAGCTCCCAAA 1 ATGGCTTCTAAAGAAATCCTTTTTGATGCTAAAGCCCCGTGAAAAACTTTCACGAGGTGTA 61 GATAAACTTGCAAATGCTGTTAAAGTAACACTTGGACCTAAAAGGCCGTAATGTCGTTATT 131 AsnGluGIYLeuLysAlaValAlaAlaGIyMetAsnProMetAspLeuLysArgGlyIle 111 AlaAsnAspAlaAlaAlaGlyAspGlyThrThrThrAlaThrValLeuAlaGlnAlaIleVal 211 SerdlyLeuGluAsnGluLeuSerValValGluGlyMetGlnPheAspArgGlyTyrLeu GATAAAGCTGTTGTTGCTGTTACTAAAGAACTAAGCGACATTACAAAGCCTACTCGTGAC ATCATAGCTGAAGCTATGGCTAAAGTTGGAAAAGGAGGTGTTATCACAGTTGAGGAAGCT 541 AAAGGICTIGAAACTACAITAGAIGIGGIIGAAGGAAIGAAGIIITGACCGIGGCIACCIC :: 121 71 181 91 241 301 361 151 421 171 481 191 à П ð g ò g Š Dp ð a ŏ g à qq δ Dp δ Dp à

267

1200 961 AAACGTGTAGTTATTGACAAAGAAAATACTATCGTTGATGGTGCTGGAAAATCAGAA 1020 1260 CGCTCCATTAAAGTCCTTGATGATATTAAACCTGCTGATGATGATGAACTTGCTGGACTT 1320 AATATCATCCGTCGTTCTTGAAGAGCCTTTACGTCAAATTGCTGCAAATGCTGGCTAT 1380 1440 CGTATTGCATTACAAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGCGCT 1560 1561 ATTGCTGAAAAACCAGAACCTAAAAAAGATATGCCTATGCCTGGCGGTGGTATGGGTGGT 1620 350 780 290 840 430 450 TTTGGTGAACGCCGTAAAGCTATGCTTGAAGATATTGCTATCCTTACTGGAGGAGAAGCA 900 TCTCCATACTTTGTAACTAATCCTGAGAAATGGTTTGTGAACTTGATAACCCTTATATC 660 471 AlaLeuLeuArgArgAlaValGluSerProLeuArgGlnIleValAlaAsnAlaGlyAsp 490 1081 GATCGTGAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCAT 391 AspargGluLysLeuGlnGluArgLeuAlaLysLeuAlaGlyGlyValAlaValIleLys ACACTTGTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGT ATATTTGAAGATCGTGGTATAAAGCTTGAAAATGTAAGCTTGTCTTTTAGGAACAGCT 331 ileSerGluGluValGlyLeuSerLeuGluGlyAlaThrLeuGluHisLeuGlyAsnAla 1141 GTTGGAGCTGCTACTGAAACTGAAATGAAAGAGAAGAAGAGGATCGTGTAGAAGATGCTCTA 451 ArgAlaLeuGlnAlaIleGluGlyLeuLySGlyAspAsnGluGluGluGlaBanValGlyIle GAAGGTTCTATTGTTGTAGAAAAGTTCGTGAACCAAAAGATGGTTTTGGATTTAATGCT CTTTGTAATGAGAAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTT GCTAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCA GATATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTAT 1201 AATGCAACAAGAGCTGCGGTTGAAGAAGGTATTGTCCCTGGTGGTGGTACTGCTTTTTGTC ---GlyGlyMetProAsp GCATCAGGAGAATATGAAGACCTTATTAAAGCTGGTGTCATTGATCCTAAAAAGTTACA ValAlaGluIleValGluAspLysProAlaMet ATGGGTGGTATGGACGGTATG 1641 MetGlyGlyMetGlyGlyMet 573 231 291 601 199 251 721 271 781 841 901 1021 411 1261 1441 1501 1621 491 511 531 1381 551

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AAY23905-30 represent heat shock proteins (Hsps). The specification describes Streptococcal Hsps, designated Hsp60. These proteins, their fragments, variants and fusion proteins, are used to elicit or enhance an immune response against Streptococcus, and to elicit a similar response to a target antigen fused to the protein. Unlike other immunological carriers, Hsp60 proteins are not immunosuppressive so provide an increased response to any conjugated or fused antigen. Also, where used for cancer control, they lack the side effects associated with endotoxins. They can also be used to detect specific antibodies and in treatment or prevention of tumours (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or liver). The Hsp60 polymucleodide is used for recombinant production of the protein, as a source of primers and probes for detecting streptococci in standard hybridization/amplification assays, and therapeutically in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding heat shock protein-60 from Streptococcus, useful in vaccines, as carriers for other immunogens, as anticancer agents and for diagnosis
                                                                                                                                                       Hsp; immune response; immunological carrier;
                                                                                                                                                                          cancer control; tumour; sarcoma; cancer; gene therapy
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Matches:
Conservative:
Mismatches:
                                                                                                                          Amino acid sequence of a heat shock protein.
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                                                                                                                                                                                                                                                                                                                                                                  (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
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                               AAY23915 standard; Protein; 545
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61.14%
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                                                                                                                                                                                                       Neisseria meningitidis.
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                                                                                              (first
                                                                                                                                                           protein;
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                                                                                                                                                                                                                                                                                                     29-DEC-1998;
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DB:
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                AAY23915
ID AAY2
RESULT 7
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61 GATAAACTTGCAAATGCTGTTAAAGTAACACTTGGACCTAAAGGCCGTAATGTCGTTATT 120

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ATGGCTTCTAAAGAAATCCTTTTTGATGCTAAAAGCCCGTGAAAAACTTTCACGAGGTGTA

US-09-077-574A-1 (1-1647) x AAY23915 (1-545)

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121 GAAAAGTCTTTTGGTTCCCCAGTTATTACAAAAGATGGTGTATCTGTTGCAAAAGAAATT 180

961 AAACGTGTAGTTATTGACAAAGAAAATACTACTATCGTTGATGGTGCTGGAAAATCAGAA 1020 1021 GATATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTAT 1080 1201 AATGCAACAAGAGCTGCGGTTGAAGAAGGTATTGTCCCTGGTGGTGGTACTGCTTTTGTC 1260 GATCGTGAAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCAT 1140 240 260 401 HisAlaThrArgAlaAlaValGluGluGlyValValAlaGlyGlyGlyValAlaLeuLeu 420 780 840 280 900 300 101 AlaGluGlyMetLysTyrvalThrAlaGlyMetAsnProThrAspLeuLysArgGly1le 120 121 AspiysalavalalaalaLeuValGluGluLeuLysAsnIleAlaLysProCysAspThr 140 141 SerLysGlulleAlaGlnValGlySerIleSerAlaAsnSerAspGluGlnValGlyAla 160 ATCATAGCTGAAGCTATGGCTAAAGTTGGAAAAGGAGGTGTTATCACAGTTGAGGAAGCT 540 009 240 GAIAAAGCIGIIGIIGCIGIIACIAAAGAACIAAGCGACAIIACAAAGCCIACICGIGAC 420 80 9 241 AlaLysAlaSerArgProLeuLeullelleAlaGluAspValGluGlyGluAlaLeuAla ACACTTGTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGT TITGGTGAACGCCGTAAAGCTATGCTTGAAGATATTGCTATCCTTACTGGAGGAAGCA GTTGGAGCTGCTACTGAAACTGAAATGAAAGAAGAAGAATGGTGTAGAAGATGCTCTA 41 AspArgAlaPheGlyGlyProHisIleThrLysAspGlyValThrValAlaLysGluIle 421 CAAAAAGAAATAGCTCAAGTTGGAACCATTTCTGCAAACTCTGATACAACAATAGGTAAT TCTCCATACTTGTAACTAATCCTGAGAAATGGTTTGTGAACTTGATAACCCTTATATC GCTAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCA 261 ThrLeuValValAsnAsnIsAsnIleArgGlyIleLeuLySThrValAlaValLySAlabroGly ATATITICAAGATCGTGGTATAAAGCTTGAAAATGTAAGCTTGTCTTCTTTAGGAACAGCT 241 ACTAGCGATATTGCTGGTGATGGAACTACAACAGCAACAGTCCTTGCACAAGCTATTTAT 301 CGTGAAGGTGTAAAACTTGTAGCAGCTGGTCGTAATCCTATGGCCATTAAACGTGGCATA AAAGGTCTTGAAACTACATTAGATGTGGTTGAAGGAATGAAGTTTGACCGTGGCTACCTC CTTTGTAATGAGAAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTT 181 GAACTTGAAGATAAGTTTGAAAATATGGGCGCTCAAATGGTTAAAAGAAGTAGCTCCCAAA 1081 301 1141 541 481 161 181 601 199 221 721 781 841 901 361 201 q g Op 임 a $\dot{\delta}$ 셤 ò à Dp 8 g ò <u>면</u> ö g ò à à qq g 원 δ q à $\overset{\circ}{\circ}$ g ð 셤 à à 8 ð à g

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represent novel Neisseria meninglis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .21 GAAAAGTCTTTTGGTTCCCCAGTTATTACAAAAGATGGTGTATCTGTTGCAAAAGAAATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GATAAACTIGCAAAIGCIGITAAAGIAACACIIGGACCIAAAGGCCGIAAIGICGIIAIT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GAACTTGAAGATAAGTTTGAAAATATGGGCGCTCAAATGGTTAAAGAAGTAGCTCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluLeuLysAspLysPheGluAsnMetGlyAlaGlnMetValLysGluValAlaSerLys
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                           AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
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2; Page 1388; 1453pp; English.
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80.88%
66.54%
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                                                                                                                           GAAGGTICTATTGTAGAAAAGTTCGTGAACCAAAAGATGGTTTTGGATTTAATGCT 1440
                                                                                                                                                                                    1441 GCATCAGGAGAATATGAAGACCTTATTAAAGCTGGTGTCATTGATCCTAAAAAAGTTACA 1500
          CGCTCCATTAAAGTCCTTGATGATATTAAACCTGCTGATGATGATGAACTTGCTGGACTT 1320
                                                                                                                                                                                                                                              CGTATTGCATTACAAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGCGCT 1560
                                                                                                                                                                                                                                                                                                              1620
                                                                   1321 AATATCATCCGTCGTTCTTGAAGAGCCTTTACGTCAAATTGCTGCAAATGCTGGCTAT 1380
                             |||::: |||||::: ||||||||::: 421 ArgAlaArgAlaAlaGlyAsnLeuHisThrGlyAsnAlaAspGlnAspAlaGlyVal 440
                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis, Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.
                                                                                            441 GlnIleValLeuArgAlaValGluSerProLeuArgGlnIleValAlaAsnAlaGlyGly
                                                                                                                                               GlySerGlyGluTyrGlyAspMetIleGluMetGlyValLeuAspProAlaLysValThr
                                                                                                                                                                                                                                                                          ArgSerAlaLeuGlnHisAlaAlaSerIleAlaGlyLeuMetLeuThrThrAspCysMet
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Scalato E, S
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Ratti
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Pizza M, Rappuoli R,
Venter JC;
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98US-0098994.
98US-0099062.
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INST GENOMIC RES.
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02-SEP-1998;
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Tettelin H,
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infection; vaccine; gene therapy

Neisseria gonorrhoeae.

WO200279243-A2

Antibacterial;

ID 1020

gonorrhoeae amino acid sequence SEQ

(first entry)

07-MAR-2003

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ThrLeuValValAsnAsnIleArgGlyIleLeuLysThrValAlaValLysAlaProGly
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                                   GCTAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCA
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of a

protein from Neisseria gonorrheae, useful for the manufacture

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Masignani

(CHIR-) CHIRON SPA.
Fontana MR, Pizza N
WPI; 2003-058415/05.

N-PSDB; ABZ38215

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GATAAACTIGCAAAIGCIGTIAAAGIAACACTIGGACCIAAAGGCCGIAAIGICGTIAIT 120
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                                                                The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins an antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP910746 ABP81046 represent nucleic acid molecules of the invention.
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medicament for treating or preventing N. gonorrheae infection
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                                   Disclosure; Page 262; 815pp; English.
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1805.50
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ABP77245 ABP77245

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protein; hsp60; GroEL protein; therapy; infection; antibiotic.
CGTATTGCATTACAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGCGCT
                                                               521 IleAlaGluIleProGluGluLysProAlaValPro---AspMetGlyGlyMetGlyGly
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treating infection caused by Francisella tularensis in an animal
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                   ThrLeuValValAsnAsnIleArgGlyIleLeuLySThrValAlaValLysAlaProGly
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                                                                     41 AspLysSerPheGlyAlaProThrIleThrLysAspGlyValSerValAlaLysGluIle
                                                                                              GAACTTGAAGATAAAGTTTGAAAATATGGGCGCTCAAATGGGTTAAAGAAGTAGCTCCCAAA
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361 AspArgGluLysLeuGlnGluArgLeuAlaLysLeuSerGlyGlyValAlaValIleLys 380
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meningitis; septicaemia;
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antigenic; diagnosis; immunogenic; infection;
antibacterial; gene therapy.
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Pizza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
Venter JC;
Petersen J,
Tettelin H,
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WPI; 2000-062150/05.

N-PSDB; AAZ54507.

Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics

Claim 2; Page 1385; 1453pp; English.

AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raisse antibodies. They may also be used to screen for agonists or antagonists, which may themselves may also be use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.

544 AA; Sequence

544 353 78 112 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 2.39e-149 1750.50 79.23% 64.89% 58.98% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB: No.:

US-09-077-574A-1 (1-1647) x AAY75745 (1-544)

04	-5/44	1-1 (1-104)) X AAY()5/45 (1-544)
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Db	Н	
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Db	41	AspargalapheGlyGlyProHisIleThrLysAspGlyvalThrValAlaLysGlulle 60
δy	181	GAACTIGAAGAITAGAAAAITAIGGGCGCICCAAAIGGITAAAGAAGIAGCICCCAAA 240
Db	61	GluLeuLysAspLysPheGluAsnMetGlyAlaGlnMetValLysGluValAlaSerLys 80
٥y	241	
Db	81	ThrasnaspvalalaglyaspglyThrThralaThrValLeualaglnSerlleVal 100
70	301	CGTGAAGGTGTAAAAACTTGTAGCAGCTGGTCGTAATCCTATGGCCATTAAACGTCGCATA 360
Db da	101	
δλ	361	GATAAAGCTGTTGTTGCTGTTACTAAAGAACTAAGCGACATTACAAAGCCTACTCGTGAC 420
Db	121	ASPLYSALAVALALAALALEUVAIGIUGIULEULYSASNIIEALALYSPIOCYSASPINI 140
òy	421	CAAAAAGAAATAGCTCAAGTTGGAACCATTTCTGCAAACTCTGATACAACAATAGGTAAT 480
qu	141	SerLysGluIleAlaGlnValGlySerIleSerAlaAsnSerAspGluGlnValGlyAla 160
٥y	481	ATCATAGCTGAAGCTATGGCTAAAGTTGGAAAAGGAGGTGTTATCACAGTTGAGGAAGCT 540
Db	161	

1621 ATGGGTGGTATG 1632

λō	541	AAAGGICITGAAACTACATTAGAIGIGGITGAAGGAATGAAGTITGACCGIGGCIACCIC 600
qq	181	LysSerLeuGluAsnGluLeuAspValValGluGlyMetGlnPheAspArgGlyTyrLeu 200
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ò	661	CTTTGTAATGAGAAAAAGATTACTAGCATGAAAGACATGATACCAATCTTAGAAAAAAAA
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ò	721	GCTAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCA 780
ΩÞ	241	AlalysAlaSerArgProLeuLeullelleAlaGluAspValGluGlyGluAlaLeuAla 260
7 0 /	781	ACACTTGTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGT 840
DP	261	ThrieuvalvalAsnAsnIleArgGlylleLeurysThrvalAlavalLysAlabroGly 280
ඊ සි	841	TTTGGTGAACGCCGTAAAGCTATGCTTGAAGATATTGCTATCCTTACTGGAGGAGAAGCA 900 THIGH
ζ	901	ATATITGAAGATCGTGCTATAAAGCTTGAAAATGTAAGCTTGTCTTTAGGAACAGCT 960
qq	301	
Qy	196	AAACGIGIAGITATIGACAAAGAAAAIACIACIATCGITGAIGGIGCIGGAAAATCAGAA 1020
QQ	321	LysarglieGluIleGlyGluGluAsnThrThrValIleAspGlyPheGlyAspAlaAla 340
č	1021	GATATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTAT 1080
QQ	341	GlnileGlualaArgValalaGluileArgGlnGlnileGluThrAlaThrSerAspTyr 360
λō	1081	GATCGTGAAAAACTICAAGAACGTCTIGCAAAACITGTIGGTGGAGTACTGTTATCCAT 1140
ପୁପ୍ର	361	AspLysGluLysLeuGlnGluArgValAlaLysLeuAlaGlyGlyValAlaValIleLys 380
δλ	1141	GTTGGAGCTGCTACTGAAACTGAAATGAAAGAAGAAGGATCGTGTAGAAGATGCTCTA 1200
qu	381	ValGlyAlaAlaThrGluValGluMetLysGluLysLysAspArgValGluAspAlaLeu 400
δλ	1201	AATGCAACAAGAGCTGCGGTTGAAGAAGTATTGTCCCTGGTGGTGGTGTTTTGTC 1260
qq	401	HisAlaThrArgAlaAlaValGluGluGlyValValAlaGlyGlyGlyValAlaLeuLeu 420
δ i	1261	CGCTCCATTAAAGTCCTTGATGATATTAAACCTGCTGATGATGATGATGATGCTGGACTT 1320
qq	421	ArgAlaArgAlaAlaLeuGluAsnLeuHisThrGlyAsnAlaAspGlnAspAlaGlyVal 440
ολ	1321	AATATCATCGGTGGTTCTCTTGAAGAGCCTTTACGTCAAATTGCTGCAAATGCTGGTAT 1380
QQ	441	GlnileValLeuArgAlaValGluSerProLeuArgGlnileValAlaAsnAlaGlyGly 460
δλ	1381	GAAGGITCIAITGITGIAGAAAAGITCGIGAACCAAAAGATGGITITGGATITAAIGCT 1440
Db	461	GluProSerValValValAsnLysValLeuGluGlyLysGlyAsnTyrGlyTyrAsnAla 480
δλ	1441	
qq	481	GlySerGlyGluTyrGlyAspMetlleGlyMetGlyValLeuAspProAlaLysValThr 500
δλ	1501	CGTATTGCATTACAAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGCGCT 1560
qq	501	ArgserAlaLeuGlnHisAlaAlaSerIleAlaGlyLeuMetLeuThrThrAspCysMet 520
λō	1561	ATTGCTGAAAAACCAGAACCTAAAAAAGATATGCCTGCCT
do é	521	<pre>11eAlaGluIleProGluGluLysProAlaValProAspMetGlyGlyMetGlyGly 539</pre>

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                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a protein that acts as a detrimental organism controller and is isolated from Enterobacter aerogenes. The invention encompasses a detrimental organism-resistant plant producing the protein of the invention in an effective amount for controlling detrimental organisms. A composition of the invention is useful for the preparation of a detrimental organism controller. The current sequence represents a detrimental organism controller protein of the invention.
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Matches:
Conservative:
Mismatches:
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1749.00
78.21%
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                                                          ABB99014 standard; protein;
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                                                                                                     (first entry)
           543
                                                                                                                                                                          Enterobacter aerogenes.
organism;
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AAACGTGTAGTTATTGACAAAGAAAATACTACTATCGTTGATGGTGCTGGAAAATCAGAA 1020
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81 AlaAsnAspAlaAlaGlyAspGlyThrThrThrAlaThrValLeuAlaGlnAlaIleVal 100
                                                                                                                                                                       481 ATCATAGCTGAAGCTATGGCTAAAGTTGGAAAAGGAGGTGTTATCACAGTTGAGGAAGCT
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                                                 301 CGTGAAGGTGTAAAACTTGTAGCAGCTGGTCGTAATCCTATGGCCATTAAACGTGGCATA
                                                                                                                                            361 GATAAAGCTGTTGCTGTTACTAAAGAACTAAGCGACATTACAAAGCCTACTCGTGAC
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                                                                                                                                                                                                                                                                                                                                              protein; flagellaless mutant; vaccine; poultry; Campylobacter.
                    GluProSerValValAlaAsnThrValLysAlaGlyAspGlyAsnTyrGlyTyrAsnAla
                                                         |||::: ||||||| ::::::|||
481 AlaThrGluGluTyrGlyAsnMetIleAspMetGlyIleLeuAspProThrLysValThr
                                                                                                                                         -GGTGGTATG
GAAGGITCTATTGTTGTAGAAAAAGTTCGTGAACCAAAAGATGGTTTTGGATTTAATGCT
                                            GCATCAGGAGAATATGAAGACCTTATTAAAGCTGGTGTCATTGATCCTAAAAAAGTTACA
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521 ValThrAspLeu------ProLysSerAspAlaProAspLeuGlyAlaAlaGlyGlyMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a 60 kba protein of Campylobacter jejuni. The protein is antigenic, and is visible on a Western blot of C. jejuni protein after incubation of the blot with antibodies against a flagellaless mutant of C. jejuni but not visible after incubation with antibodies against wild type C. jejuni. The proteins are used to produce vaccines which are useful for protecting animals, especially poultry, against Campylobacter, especially C. jejuni.
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                                                                                                                                                                                                                                                                                                                       Amino acid sequence of a 60 kDa protein from Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel Campylobacter antigenic proteins, useful for the production vaccines for protecting poultry form Campylobacter infection -
                                                                                                                                       ATTGCTGAAAAACCAGAACCTAAAAAAAAATATGCCTATGCCTGGC-----
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Length:
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Conservative:
Mismatches:
Indels:

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> Percent Similarity: Best Local Similarity: Query Match:

Score:

Gaps: (1-545)

(1-1647) x AAB19080

US-09-077-574A-1

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1027 AAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTATGATCGT 1086
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                                                                                                                                                                                                                   GAAGATAAGTTTGAAAATATGGGCGCTCAAATGGTTAAAGAAGTAGCTCCCAAAACTAGC 246
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IleAsnAspGluLeuAsnValValGluGlyMetGlnPheAspArgGlyTyrLeuSerPro
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                                                                       CTTGCAAATGCTGTTAAAGTAACACTTGGACCTAAAGGCCGTAATGTCGTTATTGAAAAG
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               GCTGCTACTGAAACTGAAATGAAAGAGAAGGATCGTGTAGAAGATGCTCTAAATGCA
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Alzheimer's disease; reconditioning; purification; inactivation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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This sequence represents the E. coli chaperone protein GroEL which can be used for treating diseases associated with protein/polypeptide structure, e.g. Alzheimer's disease. The sequence can also be used for reconditioning molecules, especially a protein that has previously been inactivated or denatured, or more generally for altering the structure of a molecule by unfolding or refolding. The sequence also has applications for purification procedures and can increase yield, specific activity or quality of biological molecules, especially by co-expression with the intranasally, or from a slow-release formulation.
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                              New chaperone polypeptide(s) derived from GroEL - useful for, e.g. refolding of proteins and for treating diseases associated with protein structure such as Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
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                                                                                                          Claim 1; Fig 7; 94pp; English.
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chaperone; großL gene

(first entry)

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97GB-0018261. 97GB-0014582.

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(MEDI-) MEDICAL RES COUNCIL.
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                                                                                       Chaperone; molecular
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                        CTTTGTAATGAAAAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTT
                                       GCTAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCA
                                                                                                                           ACACTTGTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGT
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The invention provides a method of providing chaperone activity in vivo, by administering to a cell a fragment of a molecular chaperone which has in vivo activity. Also provided is a method of determining whether a fragment of a molecular chaperone is active in vivo by: (i) providing a cell with a deficient molecular chaperone activity; (ii) administering complements the fragment complements the deficient endogenous molecular chaperone. The method can determine which fragments of the molecular chaperone can be used to complement a mutent or deficient molecular chaperone can be used to allows an in vivo assessment of chaperone activity as compared to previous tests which only measured activity in vitro.
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In vivo assay for the detection of chaperone fragment activity -useful for, e.g. complementing a molecular chaperone defect in vivo
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AAW95001 standard; Protein; 548 AA

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

January 29, 2004, 12:47:27; Search time 2467 Seconds (without alignments) 16225.972 Million cell updates/sec Run on:

US-09-077-574A-1 1647 Title: Perfect score:

1 atggettetaaagaaateet.....gtatggaeggtatgtaetag 1647 IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

22781392 seqs, 12152238056 residues Searched:

45562784 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

EST:*

gb_est1:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		AY109623 Zea mays	BC047350 Homo sapi	AK088844 Mus muscu	AY104969 Zea mays
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ALIGNMENTS

linear HTC 17-0CT-2002	Eukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta, Spermatophyta; Mamoliophyta; Liliopsida; Poales; Poaceae, PACCAD cide; Panicoideae, Andropogoneae, Zea. Chaes 1 to 2265 	.M., Whitsitt,M.S., Tingey,S.V. quences for Design of		ject, University of	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
2265 bp mRNA sequence.	ae; Streptophyta; E ophyta; Liliopsida; dropogoneae; Zea.	Miao, G.H., Vogel, J ., Morgante, M. and DuPont Consensus Se) Maize Mapping Pro 65211, USA	in getting correspo ilable from ZmDB an emap.org; ZmDB, www www.ncbi.nlm.nih.g
AY109623 Zea mays CL2221_1 mRNA sequence. AY109623 AY109623.1 GI:21213414 HTC. Zea mays Eamays	Eukaryota, Viridiplantae, Streptophyta, Spermatophyta, Magnoliophyta, Liliopsid Clade, Panicoideae, Andropogoneae, Zea. 1 (bases 1 to 2265)	Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes	Unpublished (2002) 2 (bases 1 to 2265) Coe, E.H.	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA	If you are interested these are publicly ava searching at MSL, maiz www.tigr.org; or NCBI,
RESULT 1 AY109623 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE		JOURNAL REFERENCE AUTHORS	Ħ	COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              350 NNNNNNNCAGATGCTGTCAAAGTGACAATGGGACCTAAGGGGGGGGATGTGTTATTGAG 409
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                                                                                                                                                                                                                                        /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by bubont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAGAAATAGCTCAAGTTGGAACCATTTCTGCAAACTCTGATACAACAATAGGTAATATC
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      maize cDNA sequences is either Virginia Walbot, Stanford or Pa
Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                              /db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 571.8; DB 11; Length 2265; Pred. No. 2.3e-123;
                                                                                                                                                                                                                                                                                                                                                                             83 others
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                                                                                                                                  /mol_type="mRNA"
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945 GAGTGAAAAATTTCTAGTATCCAGTCCATTGTACCTGCTCTTGAAATTGCCAATGC 1004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATCATCCGTCGTTCTTCTTGAAGAGCCTTTACGTCAAATTGCTGCAAATGCTTGGTTGA 1382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    846 IGAACGCCGTAAAGCTAIGCTTGAAGATAITGCTATCCTTACTGGAGGAGAAAATATT 905
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                                                                                                                                                                                                   CAGTTGAGGAAGCTAAAGG
                                                                                                                                                                                                                                                            765 CTCTGATGCAATGAAAAAGTTGGAAGAAAGGGTGTCATCACAGTAAAGGATGGAAAAAC
                                                     AGAAATAGCTCAAGTTGGAACCATTTCTGCAAACTCTGATACAACAATAGGTAATATCAT
                                                                                                                 705 AGAAATTGCACAGGTTGCTACGATTTCTGCAAACGGAGACAAAGAAATTGGCAATATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               606 ATACTTTGTAACTAATCCTGAGAAAATGGTTTGTGAACTTGATAACCCTTATATCCTTTG
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                                                                                                                                                                                                                                                                                                                            TCTTGAAACTACATTAGATGTTGAAGGAATGAAGTTTGACCGTGGCTACCTCTCC
                                                                                                                                                                                                                                                                                                                                                                                               825 ACTGAATGAATTAGAAATTATTGAAGGCATGAAGTTTGATCGAGGCTATATTTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               885 ATACTTTATTAATACATCAAAAGGTCAGAAATGTGAATTCCAGGATGCCTATGTTCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      666 TAATGAGAAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTTGCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1005 TCACCGTAAGCCTTTGGTCATAATCGCTGAAGATGTTGATGGAGAAGCTCTAAGTACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             786 IGTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGTTTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1065 CGTCTTGAATAGGCTAAAGGTTGGTCTTCAGGTTGTGGCAGTCAAGGCTCCAGGGTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           906 TGAAGAICGIGGIA---INAAAGCIIGAAAAIGIAAGCIIGICIITIAGGAACAGCIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1185 AGAAGAGGATTGACCCTGAATCTTGAAGACGTTCAGCCTCATGACTTAGGAAAAGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           963 ACGIGTAGTTATTGACAAAGAAATACTACTATCGTTGATGGTGCTGGAAAATCAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1083 TCGTGAAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGAGCTGCTACTGAAACTGAAATGAAAGAAGAAGAAGGATCGTGTAGAAGATGCTCTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1023 TATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     465 AAAAGATAAATACAAGAACATTGGAGCTAAACTTGTTCAAGATGTTGCCAATAACACAAA 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              584
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                               Submitted (28-FEB-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 26 Row: h Column: 17 This clone has the following problem: no 5' EST match. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="Brain, anaplastic oligodendroglioma with lp/19q loss"
| lp/19q loss" | CGAP Brn67" | /lab höst="WH10B" | /note="Vector: pCMV-SPORT6" | /note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: ang@bcm.tmc.edu
Gunaxatne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 TICTAAAGAAATCCTTTTTGATGCTAAAGCCCGGTGAAAAACTTTCACGAGGTGTAGATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     405 GAGTTGGGGAAGTCCCAAAGTAACAAAGATGGTGTGACTGTTGCAAAGTCAATTGACTT
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                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: David N. Louis, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 7.5e-110;
0; Mismatches 696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4214709"
                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                             Contact: MGC help desk
                                   Mammalia; Eutheria; )
1 (bases 1 to 2409)
                                                                                                                                              Direct Submission
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                                                                                                          Strausberg, R.
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Adachi, J., Alizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, M., Hiranch, T., Hiraoka, T., Hiraoka, T., Hiraoka, T., Kosanida, K., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kawai, J., Kojima, T., Miyazaki, A., Murata, M., Okaza, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saito, R., Sakai, K., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tanaka, T., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Taya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Toyaru, A., Toya, T., Yasunishi, A., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LILADAYAYTMGFKGATY IIEQSWGSFKYTKOGYTVAKKSIDLKOKYKNIGAKLVQDVA
NNTNEEAGDGTTTATVLARSIAKEGFEKISKGANFVEIRKGWTAVDAYATAEKJKOSK
PYTTPEEIAQAYATISANGDKOIGNIISDAMKKYGRKGVITVKDGKTLNDELEIIEGMK
PYTTPEEIAQAYTISANGDKOIGNIISDAMKKYGRKGVITVKDGKTLNDELEIIEGMK
PYTTPEEIAQAYTISANGDKORPODAYVLLSEKKISSVOSIVPALEIANAHKKPLYIIAE
DVDGEBALSTLVLNTEKYGLQVVAVKAPGFGDNRKNQLKDMAIATGGAVFGEEGLNLNI
EDVQAHDLGKYGEVIVTKDDAMLLKKGRDEAHIERROLDITTSPEKEKKLNE
RILAKLSDGVAVLKYGGTSDVEVNEKKORVTDALNATRAAVEEGIVLGGGGALLKCIPE
DDSLKPAREDQKIGTEIIKKAALKIPAMTIAKNGRVEGSLIVEKILLGSSSEVGYDAMLG
DFVNMVEKGIIDPTKVVRTALLDAAGVASILTTAEAVVTEIPKEEKDPGMGAMGGMGG
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| Call type="thymic cells"
| tissue type="thymis"
| clone lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="unnamed protein product; heat shock protein, 60 kDa
(MGD|MGI:96242, GB|X53584, evidence: BLASTN, 98%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MLRLPTVLRQMRPVSRALAPHLTRAYAKDVKFGADARALMLQGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Shysical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics edelloome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                         Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2246)
                                                                                                                                                                                                          The FANTOM Consortium and the RIKEN Genome Exploration Research
annotation of a full-length mouse cDNA collection
(6821), 685-690 (2001)
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/strain="NOD"
/db_xref="FANTOM DB:E430028C20"
/db_xref="taxon:10090"
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Location/Qualifiers
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/db_xref="G1:26353954"
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                                            1503 TATTGCATTACAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGCGCTAT 1562
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1263 CICCATIAAAGICCIIGAIGAIAIITAAACCIGCIGAIGAIGAIGAACIIGCIGGACIIAA 1322
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Hainey,C.F., DoLan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design
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                                                                          1072 ACTATCCTGGAGGATGCTATTAGAAGTGGATATCCAATTCTAATAGTGGCAGAGGACATT 1131
                                                                                                                                                                        GAGCAGGAAGCTCTTGCAACCCTTGTGGTTAATAGGCTTAGAGGTGCATTGAAGATTGCT 1191
                                                                                                                                                                                                                                                                          GCTATTAAGGCCCCTGGTTTTGGAGAGCGCAAAAGTCAATATCTTGATGACATTGCTACT 1251
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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               Missouri, Columbia, MO 6211, USA

If you are interested in getting corresponding physical clones, these are publicly available from ZamB and may be found by BLAST searching at MSL, maisemap.org; ZamBB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat www.zmdb.iastate.edu.
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Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
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1259 CTTGGATGATATTGCCATCCTTACTGGAGCAACTGTAATCAGAGATGAAGTTGGGCTGTC
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                                                                                                                                                959 GITGIGGAGGGAAIGCAAITIGACCGIGGITACAICTCTCCGTACITIGIAACAGACAGI
                                                                                                                                                                                                                                                           1019 GAGAAAATGTCTGCCGAGTATGAGAACTGCAAGCTGCTTTTGGTTGACAAAAAGATCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                               744 TATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCAACACTTGTAGTCAATAAGCTCCG
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                                                                                                                                                                                                       GAGAAAATGGTTTGTGAACTTGATAACCCTTATATCCTTTGTAATGAGAAAAAGATTACT
                                                                                                                                                                                                                                                                                                                  685 AGCATGA-AAGACATGCTACCAATCTTAGAACAAGTTGCTAAAGTAAACCGTCCACTCCT
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                                                                                                                                                                                                                                                                                     Submitted (22-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BiAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or MCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat.
Schnable, Lowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 GAIGGGICAGCIATCAAGAAGCICCAGACIGGAGICAAIAAGCIIGGAGACCIAGIIGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 ATTACAAAAGATGGTGTATCTGTTGCAAAAGAAATTGAACTTGAAGATAAGTTTGAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u> Arrettaacearegecertacaerrecaacaegaecricaaceaecerecrerereaaac</u>
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                                        1 (bases 1 to 2338)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 2338;
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Pred. No. 4.1e-97;
0; Mismatches 633;
                       clade; Panicoideae; Andropogoneae; Zea
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/db_xref="MaizeDB:633377"
/db_xref="taxon:4577"
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Best Local Similarity 58.0%;
Matches 893; Conservative
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                                                                         361 GGACTCAAGGTATGTGCTGTCAAAGCTCCTGGATTTGGTGAAAATAGAAGGCACAATCTA 420
                                                                                                                                                                                                                        GAAAATGTAAGCTTGTCTTTAGGAACAGCTAAAACGTGTAGTTATTGACAAAGAAAAT 987
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 2143)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
                            808 GCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGTTTTTGGTGAACGCCGTAAAGCTATGCTT
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                                                                                                                                                                     GATGACATGGCTGTGATGACTGGAGGAGGTTATTAGCGAGGAACGCGGTCTTGATCTT
                                                                                                                                                                                                                                                                                                                       988 ACTACTATCGTTGATGGTGCTGGAAAATCAGAAGATATTAAAGCTCGAGTTAAACAAATT
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                                                                                                                          GAAGATATTGCTATCCTTACTGGAGGAGAAGCAATATTTGAAGATCGTGGTATAAAGCTT
                                                                                                                                                                                                                                                                         GGCAAAGTTCAATTACAAATGCTTGGCACTGCTAAAAAAGGTAACTGTATCCCTTGATGAT
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AY108560.1 GI:21211654
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If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.rmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnabbe, Iowa State, then clones may be requested from ZmDB:

www.zmdb.iastate.edu.
                         HTC 16-0CT-2002
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                                                                                                                                                                                                                                                        Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Maize Mapping Project/DuPont Consensus Sequences for Design of
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Zea mays PC0128697 mRNA sequence.
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                 TTTGAGACCACAGTTGAAGTTGAAGAGGGATGGAGCTTGACAGAGGATATATCTCCCCT
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If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat www.zmdb.iastate.edu.
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      Maize Mapping Project/DuPont Consensus Sequences for
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   563 Arcirgargaagaagcrciraagrackcrcgrcrrgaaragcraaaggrrggrcrrcagg
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                 383 idaagirirgarcdaggcrararrichccaracrirarraaracarcaaaaggrcagaaar
                                                                                                                                                                                                                                                                                                            TGCTACCAATCTTAGAACAAGTTGCTAAAGTAAACCGTCCACTCCTTATTATTGCTGAAG
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TGAAGTTTGACCGTGGCTACCTCTCTCCATACTTGTAACTAATCCTGAGAAAATGGTTT
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/clone="C80DG003N066"
/tissue type="B CELLS (RAMOS CELL LINE)"
/cell line="RAMOS CELL LINE"
/clone lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/clone lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/note="Vector: pcMVSPORT 6; lst strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pcMVSPORT 6 vector. Library was not normalized."
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Li W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length, cDNA libraries and normalization
                                                     ALS59862 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens CDNA clone CSODG003XN06 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1228.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DG003DG03QP1&cluster=1228.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fullength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DG003DG03QP1.
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57.4%; Pred. No. 2e-71;
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Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
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841 TCACCGTAAGCCTTTGGTCATAATCGCTGAAGATGTTGATGGAGAAGCTCTAAGTACACT 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1327 bp DNA linear GSS 01-MAY-20 LLMGtag372 MG1363 Random Sequence Tag Library Lactococcus lactis subsp. cremoris genomic, genomic survey sequence.
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                                                                   786 TGTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAAGCTCCTGGTTTTGG
                                                                                                                                          901 CGTCTTGAATAGGGCTAAAGGTGGTCTCCAGGGTGTGGCAGTCAAGGCTCAGGGTTTTTGG
                                                                                                                                                                                                                 846 TGAACGCCGTAAAGCTATGCTTGAAGATATTGCTATCCTTACTGGAGGAGAAGCAATATT
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292 c 239 g 403 t lothers
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/clone_lib="MG1363 Random Sequence Tag_Library"
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Bolotin,A., Bhrlich,S.D. and Sorokin,A.
Studies of genomes of dairy bacteria Lactococcus lactis
Sci. Aliments, (2002) In press
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/organism="Lactococcus lactis subsp. cremoris"
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65.7%; Pred. No. 1.7e-64;
ive 0; Mismatches 256; Indels
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Lactococcus lactis subsp. cremoris
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                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="MG1363"
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Submitted (15-ARR-2002) Maize Mapping Project, University of Submitted (15-ARR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA.

If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu, TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize CDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB:
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Unpublished (2002)
2 (bases 1 to 1387)
Coe, E.H.
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/organism="Zea mays" Location/Qualifiers 1. .1387 /mol_type="mRNA"

www.zmdb.iastate.edu.

source

FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                               /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs, this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 AGCCACTGTTGAAGTTGAAGAATGGAGATTGACCGCGGTTATTTTCCCCACAATT
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Library"
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xref="MaizeDB:637188"
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846 TGAAGTGGTTGTGGGAAGATCAGAGAGGGGGGGGGGGGG	- 4 E E	inidae; Homo. gi:12778755. scope.cns.fr a division of	Invitrogen. This sequence belongs to sequence cluster 1228.r For http://www.genoscope.cns.fr. http://www.genoscope.cns.fr. cgi-bin/cluster.cgi?seq=CLOBB016ZA04RP1&cluster=1228.r. Contact : feng Liang Parin'cluster=1228.r. Contact : Feng Liang End : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CLOBB016ZA04RP1. Location/Qualifiers 1.1172 /organism="Homo sapiens" /nol_type="MRNA" /clone="Tubor = "NEUROBLASTOMA" /clone="Tubor = "Vector: pOWVSPORT 6; lst strand CDNA was primed	with a worl-oligo(UI) primer. Frve prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized." 352 a 216 c 293 g 294 t 17 others	tch al Similarity 59.9%; Pred. No. 5.4e-64; 543; Conservative 4; Mismatches 357; Indels 2; Gaps 1; 6 TTCTAAAGAAATCCTTTTGATGCTAAAGCCCGTGAAAAACTTTCACGAGGTGTAGATAA 65	66 ACTIGGAAAIGCIGITAAAGIAACACITGGACCIAAAGGCCGIAAIGICGIIAIIGAAAA 125
5	RESULT 12 AL515262 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES	BASE COUNT ORIGIN	Query Match Best Local S Matches 543 Qy 6	Qy 66

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944 CGTCTTGAATAGGCTAAAAGTTGGTCTTCAGGTTGTGGCAGTKAAGGCTCCAGGGTTTGG 1003
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1004 TGAM--ATAGAAAGAACARCTTAAAGATATGGCTATTGCTACTGGTGGTGGTGTTTTG 1061
                                                                                                                                                                                                                                                                   246 CGATATTGCTGGTGATGGAACTACAACAGCAACAGTCCTTGCACAAGCTATTTATCGTGA 305
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GICTITIGGIICCCCCAGIIAITACAAAAATGGIGIAICTGIIGCAAAAGAAATIGAACI 185
                                             284 GAGTIGGGGAAGTCCCAAAGTAACAAAGATGGTGTGACIKITGCAAAGTCAATIGACIT 343
                                                                                                                                                                                                344 AAAAGATAAATACAAAAACATTGGAGCTAAACTTGTTCAAGATGTTGCCAATAACAAAA 403
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Li.W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     524 AGCIGITGAIGCIGITATIGCIGAACTIAAAAAGCAGITIAAACCIGITACCACCCCIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      584 AGAAATTGCACAGGTTGCTACGATTTCTGCAAACGGAGACAAAGAAATTGGCAATATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    786 IGTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGTTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       426 AGAAATAGCTCAAGTTGGAACCATTTCTGCAAACTCTGATACAACAATAGGTAATATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          546 TCTTGAAACTACATTAGATGTGGATTGAAGGAATGAAGTTTGACCGTGGCTACCTCTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      726 AGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCAACACT
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/tissue type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/nche="Vector: pCMVSPORT_6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and BcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
1 227 c 290 g 290 t 46 others
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                              665
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                                                                                                                                                                                                                                                  849 GAGTGAAAAGAAATTTCTAGTATCCAGTCCATTGTACCTGCTCTTGAAATTGCCAATGC 908
                                                                                                                                                                                                                                                                                                                                                                                                     TCACCGTAAGCCTTTGGTCATAATCGCTGAAGATGTTGATGGAGAAGCTCTAAGTACACT 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For
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cgi-bin/cluster.cgi?seq=CSODE012AB06QP1&cluster=1228.r. Contact
                                                                                                                                                                             TAATGAGAAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTTGCTAA
                              ATACTTTGTAACTAATCCTGAGAAAATGGTTTGTGAACTTGATAACCCTTATATCTTTG
                                                                                                    789 ATACTTTATTAATACATCAAAAGGTCAGAAATGTGAATTCCAGGATGCCTATGTTCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGTTTTGG
                                                                                                                                                                                                                                                                                                                            726 AGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCAACACT
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODE012AB06QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1228.r l
more information about this cluster, see
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Li.W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.0%; Score 312.6; DB 13; 58.0%; Pred. No. 1.6e-62; tive 18; Mismatches 353; I
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/db_xref="taxon:9606"
/clone="CS0DE012YC11"
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BX439563
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/db xref="taxon:9606"
/clone="csobao09Y115"
/tissue type="wRUROBLASTOWA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 GAGTTGGGGAAGTCCCAAAGTAACAAAGATGGTGACTGTTGCAAAGTCAATTGACTT 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reccadadarchadarringerecadarecceaecerradicerreadereradacer 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 ACTIGCAAAIGCIGITAAAGTAACACTIGGACCTAAAGGCCGTAAIGICGTIAIIGAAAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 TITAGCCGATGCTGTGGCCGTTACAATGGGGCCAAAGGGAAGAACAGTGATTATTGAGCA 308
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                                                                                                                                                                                                                                                              For
                                                                                                                                                                                                                                                                                                                                   http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSODA009AE08D1&cluster=1228.r. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODA009AE08QP1.
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                                                                                                                                          Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1228.r
more information about this cluster, see
                                      2001 this sequence version replaced gi:12782125.
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Contact: Genoscope
Genoscope - Centre National de Sequencage
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  TICTAAAGAAATCCTTTTTGATGCTAAAGCCCGTGAAAAACTTTCACGAGGTGTAGATAA
                                            TGCMAAARATGTAAAATTTTGGTGCAGATGCCCGAGCMTTAATGCTTCAAGGTGTAGACCT
                                                                                        66 ACTIGCAAAIGCIGITAAAGIAACACTIGGACCIAAAGGCCGIAAIGICGITATIGAAAA
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arboreum cDNA clone GA_
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SOURCE ORGANISM

VERSION KEYWORDS

DEFINITION

RESULT 15 BF275584

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

i eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

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wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber

L Unpublished

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="GA_Eb0024G23f"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Iab host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
1 157 c 219 g 245 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              522 TATCACAGTIGAGGAAGCTAAAAGGICTIGAAACTACATTAGAIGIGGTIGAAGGAAIGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 GTTTGAGAATGCAAGAGTGTTGGTAACTGATCAAAAGATTTCAGCTATAAAAGACATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 TCCCCTGTTAGAAAAGACCACTCAATTAAGATCTCCTTTGCTTATAATTGCTGAGGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCCGTAAAAGCTCCTGGTTTTTGGTGAACGCCGTAAAGCTATGCTTGAAGATATTGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        377 AGCCATTAAAGCTCCTGGTTTTGGTGAAAGGAGAAAAGCTCTCCTTCAAGATATTGCCAT
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Pred. No. 1.7e-62;
0; Mismatches 306; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Gossypium arboreum"
                                                                                                                                                                                                                                                                                                                        Email: rwing@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
High quality sequence stop: 716.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="8400"
/db_xref="taxon:29729"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="AKA"
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Best Local Similarity
Matches 494; Conserv
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COMMENT
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1002 TGGTGCTGGAAATCAGAAGTATTAAAGCTGGGTTAAACATTGGTGCACAAATTGA 1061

Db

1062 AGAACAAGCTCAAAGGATGAGATACANACTAAGGAGCAACTAAAAAAGAGCTAGC 616

Oy

1062 AGAACAAGCTCAGATTATGATCGTGAAAACTTCAAGAACTTGCAAACTTGTTGG 1121

Db

1122 TGGAGTACTCTTTATCAGAAAATTGGCAGAAGGATTGCCAAACTTCTGG 676

Oy

1122 TGGAGTAGCTTATCCATGTGGAGCTGCTACAAAAATGAAAGGATTGCCAAACTATCTGG 676

Oy

1122 TGGAGTAGCTTATCAGAAAATTGAAAAATGAAAGGATTGTCGAAACTATCTGG

Oy

1124 TGGTGTTGGAGTAGTTAAAGGTGGAGGCTGCAACTAGAAGGATTGTCGCTGG 1241

Db

737 ACGGATTGAAAAGATGCTAAATGCAACAAGAACTTGAAGGTTTGTCGCTGG 1241

Db

737 ACGGATTGAAAAGATGCTAAATGCAACAACAAGAACTTGAAGGTTTGTGCCTGG 1261

Db

737 ACGGATTGAAAGATGCTAAATTGCTGCTGCCATAGNAAAGATTGTGCCTGG 796

Oy

1242 TGGTGGTGCTTTTGTCC 1261

Db

737 TGGTGGTGCTTTTGTCC 1261

Db

737 TGGTGGTGCTTTTGTCC 1261
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Search completed: January 29, 2004, 15:25:33 Job time : 2474 secs

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January 29, 2004, 14:44:13; Search time 475 Seconds (without alignments) 12637.020 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 1, Appli	Sequence 1, Appli	Sequence 33982, A	Sequence 1, Appli	Sequence 40819, A	Sequence 42, Appl	Sequence 1, Appli	Sequence 50, Appl	Sequence 380, App	Ċ	. 92	Sequence 26, Appl		26,	Sequence 26, Appl
ΩΙ	US-10-228-167A-1		US-10-369-493-33982	US-09-790-988-1	US-10-369-493-40819	US-09-070-927A-42	US-10-289-762-1	US-10-267-311-50	US-09-841-132-380	US-09-960-428-13	US-10-157-317-26	US-10-157-339-26	US-10-157-305A-26	US-10-157-391-26	US-10-157-096-26
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% Query Match Length DB	1635	14.1 1830121	1626	640681	1635	3625	1230025	1926	1635	2155	3840	3840	3840	3840	3840
% Query Match	44.9	44.1	43.6	43.1	42.6	42.4	41.9	41.9	41.9	41.6	41.6	41.6	41.6	41.6	41.6
Score	739.4	725.8	718.2	710	701.4	698.4	690.2	689.8	689.6	684.4	684.4	684.4	684.4	684.4	684.4
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Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	· Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence
LO-157- LO-157- LO-154-	US-10-157-299-26 US-10-156-831-26	US-10-156-902-26 US-10-157-147-26	10-157-166-2	10-157-	US-10-156-811-26 US-10-157-320A-26	-157-418A-2	US-10-369-493-46781	US-10-369-493-33701	10-369	2	9-882-227-41	-10	09-841-260-1	10-007-693-1	0-369-493-	5	0-369-4	US-10-369-493-43871	-10 - 369	10-369-493	10-369-493-3	US-10-369-493-39904	US-10-032-585-6410	US-10-369-493-39525
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41.6 41.6 41.6	41.6	41.6	41.6	41.6	41.6	41.6	41.5	41.3	41.3	39.1	38.8	38.7	38.2	38.2	37.8	36.9	36.7	35.7	35.5	34.2	34.0	34.0	33.6	•
684.4 684.4 684.4	684.4	684.4 684.4	684.4	684.4	684.4	684.4	683.8	681	8.089	643.8	639.2	637.4	629.2	629.2	623.2	607.6	604.4	587.4	585.2	563.4	260	260	53	551.8
16 17 18	13	21 22	23	24	2 2	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: Hernan Marshall Gonzalez, Sergio
TITLE OF INVENTION: HIGHLY IMMUNOGENIC PROTEIN AGAINST THE INTRACELLULAR PATHOGEN AGER
TITLE OF INVENTION: HIGHLY IMMUNOSENIC PROTEIN ARICH AFFECTS SALMON CULTURE, AMINO ACI
TITLE OF INVENTION: ACID SEQUENCES OF SALD PROTEIN AND ITS APPLICATION IN THE DEVELOR
TITLE OF INVENTION: METHODS FOR THE PREVENTION AND DIAGNOSIS OF DISEASES CAUSED BY SF
FILE REFERENCE: 076502-9004
CURRENT APPLICATION NUMBER: US/10/228,167A
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: Chilean Patent Application No. US20030147909A1 2086-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGCTTCTAAAGAAATCCTTTTTGATGCTAAAGCCCCGTGAAAAACTTTCACGAGGTGTA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.9%; Score 739.4; DB 13; Length 1635; 66.2%; Pred. No. 2.7e-141; tive 0; Mismatches 546; Indels 9;
                        ; Sequence 1, Application US/10228167A; Publication No. US20030147909A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
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Matches 1086; Conservative
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US-10-228-167A-1
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OY 1261 CGCTCCATTAAA DD 1261 CGCGCATGGC QY 1321 AATATCATCGT DD 1321 AACATCTTGTT QY 1381 GAAGGTCTATT QY 1381 GAAGGTCTATT QY 1381 GAAGGTCTATT QY 1441 GCATCAGGAGA QY 1501 CGTATTGCATT QY 1501 CGTATTGCATTG QY 1501 CGTATTGC	; ORGANISM: Haemophilus FEATURE: ; NAME/KEY: misc feature LOCATION: (4747)(47477)(474777)(47477)(47477)(47477)(47477)(47477)(47477)(47477)(47477)(47477)(47477)(47477)(47477)(47477)(47477)(47477)(47477)(47477)(47477)(474777)(474777)(474777)(474777)(474777)(4747777)(4747777)(4747777)(47477777)(4747777777)(4747777777777
	901 ATCICTGAAGAAGTIGGCCTAGAGAAGCAACTCTTGAGCACTTAGGTACAGCA 960 961 AAACGTGTGTTATTGACAAAGAAATCTACTATCATGATGGTGCTGAAAAT 1020 961 AAACGTGTGTGTTATTGACAAAGAAATACTACTATTGATGGTGCTGGAAAATT 1020 1021 GATATTAAAGCTCGTTAAAGACAATTCGTGCAAATTGATGAGGTGCGGTGAAAAT 1020 1021 GATATTAAAGCTCGGTTAAACAAATTCGTGCAAATTGAAGAAACAAAAT 1080 1081 GATCGTGAAAAACTTCAAAAACTTCGAAAATTGATGAGAGAAACATCCTCTGACTAC 1080 1081 GATCGTGAAAAACTTCAAAAACTTCGAAAACTTGAAGAAAAAAAA
2 4 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5	B & B & B & B & B & B & B & B & B & B &

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ucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag
Thereof, and Uses Thereof
                        CTGCAGTTAAAGCTCTTGACTTCGCAAATGATGAACAAGCCCAAGGTGCT 1320
                                                         AAGTCCTTGATGATATTAAACCTGCTGATGATGATGAACTTGCTGGACTT 1320
                                                                                                                    TTGTTGTAGAAAAAGTTCGTGAACCAAAAGATGGTTTTGGATTTAATGCT 1440
                                                                                                                                            TAATTCTTGATAAATTGTCAACGGTGAAGGTAACTTTGGTTATAATGCA 1440
                                                                                                                                                                          AATATGAAGACCTTATTAAAGCTGGTGTCATTGATCCTAAAAAGTTACA 1500
                                                                                                                                                                                                TACAAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGCGCT 1560
                                                                                                                                                                                                                                                          AACCAGAACCTAAAAAAGATATGCCTATGCCTGGCGGTGGTATGGGTGGT 1620
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NUMBER: US/10/329,960
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MBER: US 09/643,990
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equals a, t, g or c
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Y: misc_feature N: (36551)(36551) NFORMATION: n equals a,	: misc feature : (366 <u>3</u> 6)(36636) FORMATION: n equals a,	: misc_feature : (40808) . (40810) FORMATION: n equals a,	: misc_feature : (44416) (44416) FORMATION: n equals a,	: misc feature : (44905) . (44905) FORMATION: n equals a,	: misc feature : (44975) (44975) FORMATION: n equals a,	: misc_feature : (45593)(45593) FORMATION: n equals a,	: misc feature : (45732)(45732) FORMATION: n equals a,	YEATURE: AME/KEY: misc_feature OCATION: (47036)(47036) DTHER INFORMATION: n equals a, 1	, a	s a,	FEATURE: WAME/KEY: misc_feature OCCATION: (51786)(51786) TTHER INFORMATION: n equals a,	: misc_feature : (51805)(51805) FORMATION: n equals a,	FRATURE: MRE/KEY: misc_feature ACATION: (55369)(55369) OTHER INFORMATION: n equals a,	: misc_feature : (65309)(65309) FORMATION: n equals a,	FEATURE: RAME/KEY: misc_feature COCATION: (653 <u>1</u> 3)(65313) 7THER INFORMATION: n equals a,	: misc_feat : (80024) FORMATION:	FEATURE; NAME/KEY: misc feature LOCATION: (100091)(100091) OTHER INFORMATION: n equals a,	NAME/KEY: misc_feature

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FEATURE:
NAME/KEY: misc_feature
LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals a, t, g or c
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LOCATION: (145942)..(145942)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
                              or c
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LCCATION: (105121)..(105121)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
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LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals a, t, g or c
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LOCATION: (119750)..(119750)
OTHER INFORMATION: n equals a, t, g or c
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LOCATION: (120038)..(120038)
OTHER INFORMATION: n equals a, t, g or c
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NAME/KEY: misc_feature
LOCATION: (122167)..(122167)
OTHER INFORMATION: n equals a, t, g or c
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NAME/KEY: misc_feature
LOCATION: (131340). (131340)
OTHER INFORMATION: n equals a, t, g or c
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NAME/KEY: misc feature
LOCATION: (131360)
OTHER INFORMATION: n equals a, t, g or c
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LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals a, t, g or c
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NAME/KEY: misc_feature
LOCATION: (139910)
CTHER INFORMATION: n equals a, t, g or PEATURE:
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NAME/KEY: misc feature
LOCATION: (117136)..(117136)
OTHER INFORMATION: n equals a, t, g or
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LOCATION: (119924)..(119924)
OOTHER INFORMATION: n equals a, t, g or
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LOCATION: (140398)..(140398)
OTHER INFORMATION: n equals a, t, g or
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LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals a, t, g
LOCATION: (102686)..(102696)
OTHER INFORMATION: n equals a, t, g
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NAME/KEY: misc_feature
LOCATION: (121344)...(121344)
OTHER INFORMATION: n equals a,
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LOCATION: (145171)...(145171)
OTHER INFORMATION: n equals a,
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LOCATION: (147197)..(147197)
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US(310/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
                                                  566190 TTTGGTGATCGTCGTAAAGCGATGTTACAAGATATTGCAATTTTAACAGGGGTACAGTG 566249
     TTTGGTGAACGCCGTAAAGCTATGCTTGAAGATATTGCTATCCTTACTGGAGAGAAGCA 900
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                                                                                                                                             566250 ATTICTGAAGAAATTGGTATGGAGCTTGAAAAAGCAACATTGGAAGATTTAGGTCAAGCA
                                                                                                                                                                                                                                             566310 AAACGTGTTGTTATCAATAAAGATAACACAACCATTATTGATGGTATCGGCGATGAAGCA
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                                                                                                    ATATTTGAAGATCGTGGTATAAAGCTTGAAAATGTAAGCTTGTCTTCTTTAGGAACAGCT
                                                                                                                                                                                               AAACGIGTAGTTATTGACAAAGAAAATACTACTATCGTTGATGGTGCTGGAAAATCAGAA
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Publication No. US20030233675A1
GENERAL INFORMATION:
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Matches 1086; Conservative
                      FEATURE:
NAME/KEY: misc_feature
LOCATION: (150841) ..(150841)
OTHER INFORMATION: n equals
                                                                                                                    FEATURE:
NAME/KEY: misc_feature
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                                                                                                                                            43.6%; Score 718.2; DB 12
65.7%; Pred. No. 5.8e-137;
                                                                    ; TYPE: DNA
; ORGANISM: Cytophaga hutchinsonii
US-10-369-493-33982
PRIOR FILING DATE: 2002-02-21
               NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 33982
LENGTH: 1626
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Pred. No. 3.1e-134;
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APPLICANT: SAKAKI, YOSHTUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
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Patent No. US20020127687A1
GENERAL INFORMATION:
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1148 CTGCTACTGAAACTGAAATGAAAGAGAGAGAGAGAGAGAG	FILING DATE: 1997-05-06 APPLICATION NUMBER: 60/066, FILING DATE: 1997-11-14 ATTORNEY/AGENT INFORMATION: NAME: Kenley K. HOOVER REGISTRATION NUMBER: 40,302
AMAGTAACACTTGGACCTAAAGGCCGTAATGTCGTTATTGAAAAGT AAAGTAACGCTAGGACCTAAAGGCCGTAACGTCGTTATTGAAAAGA STATTACAAAAGATGGACCTAAACGTCGTACGTTCTTGTAAAAGA AAAATTGGCCGCTCAAATGGTTAAAGAACTTGCAAAATTGAAATTGC AACATGGGTCCAAATGGTTAAAGAACTGCCAAAGAATTGAAATTGC SGAACTACAACAACAGCTGTTGCAGAACTGCAAACAAAAGAAATTGAAAAG SGAACTACAACAACAACAGTTGTTGCAGAAATTGAAATTGCAAAAGAAATTGCAAAAGAAATTGCAAAAGAAATTCGTAAAGAAATTCGCAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAA	1022 CAGCTCGCGTTAATCAAATCAAAGCACAAATCGAAAACAACATCTGACTTCGATAAAG 1081 1088 AAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCATGTTGGAG 1147 1082 AAAAACTTCAAGAGCGCTTAGCAAGCTTGCTGGTGGCGTCGCTGTTCTTAAAGTCGGTG 1141
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                                                                                                                                                                                                  Score 698.4; DB 10; Length 3625;
Pred. No. 8.9e-133;
0; Mismatches 527; Indels 6;
                                                                                                                                                        42:
REFERENCE/DOCKET NUMBER: PB369
                                                                                                                         ; TOPOLCGY: linear; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-070-927A-42
                             301) 309-8504
(301) 309-8512
              TELECOMMUNICATION INFORMATION:
                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 3625 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                          INFORMATION FOR SEQ ID NO: 42:
                                                                                                                                                                                                  Query Match
Best Local Similarity 66.1%;
Matches 1040; Conservative
                           TELEPHONE:
                                             TELEFAX:
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APPLICANT: Griffals, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
CURRENT APPLICATION UNBER: US/10/289,762
CURRENT APPLICATION UNBER: 2003-03-27
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 1230025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTTACAAAATGCAGCTTCTGTGTCAGCTTTATTATTAACAACTGAAGCAGTTGTTGCAG 1921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1385 ATGCCCGCGTTCATTTAATTAAAAACCAAAATCGGCGAAACAACGTCTGATTTTGATCGTC
                                                                                                 AAGATCGTGGTATAAAGCTTGAAAATGTAAGCTTGTCTTCTTTAGGAACAGCTAAACGTG
                                                                                                                                                                                              ACGACTTAGGGTTAGAGTTAGAGACACAACTATTGAAAACTTTAGGAAATGCTAGCAAAG
                                                                                                                                                                                                                                                                                                     TAGTTATTGACAAAGAAAATACTACTATCGTTGATGGTGCTGGAAAATCAGAAGATATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1028 AAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTATGATCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1445 AAAAATTACAAGAACGTTTAGCTAAATTAGCTGGTGGGGGTTGCTGTCGTTAAAGTCGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGAATATGAAGACCTTATTAAAGCTGGTGTCATTGATCCTAAAAAAAGTTACACGTATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1565 CACGIGCCCCIGIAGAAGAAGCAIGGITICIGGIGGIAGCIACCGCACIGGICAAIGIAA
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NAME/KEY: misc feature LOCATION: (240001)..(255000) OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (25501)..(270000) OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (270001)..(285000) OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc_feature LOCATION: (45001)..(60000) OTHER INFORMATION: n=a or c or g or FRATURE:
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OTHER INFORMATION: n=a or c or g or or NAME/KEY: misc feature LOCATION: (105001)..(120000) OTHER INFORMATION: n=a or c or g or or NAME/KEY: misc_feature LOCATION: (150001)..(165000) OTHER INFORMATION: n=a or c or g or or NAME/KEY: misc feature LOCATION: (210001)..(225000) OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature LOCATION: (22501)..(24000) OTHER INFORMATION: n=a or c or g or OTHER INFORMATION: n=a or c or g or or οĸ or or or NAME/KEY: misc feature LOCATION: (120001)..(135000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (180001)..(195000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc_feature LOCATION: (195001)..(210000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (15001)..(30000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (60001)..(75000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (90001)..(105000) OTHER INFORMATION: n=a or c or g p NAME/KEY: misc feature LOCATION: (30001)..(45000) OTHER INFORMATION: n=a or c or NAME/KEY: misc feature LOCATION: (135001)..(150000) OTHER INFORMATION: n=a or c or NAME/KEY: misc_feature LOCATION: (165001)..(180000) OTHER INFORMATION: n=a or c or FEATURE:

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LOCATION: (540001)...(555000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (345001)..(360000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (285001)..(300000)
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LOCATION: (480001)..(495000)
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LOCATION: (300001)..(315000)
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LOCATION: (37501)..(390000)
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LOCATION: (390001)..(405000)
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LOCATION: (510001)..(525000)
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LOCATION: (31501)..(330000)
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LOCATION: (360001)..(375000)
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LOCATION: (405001)...(420000)
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LOCATION: (420001)..(435000)
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LOCATION: (43501)..(450000)
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LOCATION: (450001)..(465000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (49501)..(510000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (52501)..(54000)
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LOCATION: (330001)..(345000)
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LOCATION: (465001)..(480000)
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178572 GTTAGCGAAGAACTTGGCATGAAACTAGAGAATACAACTCTAGCAATGTTAGGAAAAGCT 178513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGACTCGCTCAGCTCTAGAAAGCGCAGCTTCTATCGCAGGATTACTCCTCACACAGAA 177913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCTGTATCCCTACACTAGAAGCTTTCCTTCCTATGCTAGCAAACGAAGACGAAGCTATT 178153
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                                                                                                                                                                           178932 AAAGGCTTCGAAACTGTTCTCGACGTTGTAGAAGGAATGAACTTCAACCGTGGATACTC
                                                                                                                                                                                                                                                                                           178872 TCCAGCTACTTCTCCACAAATCCAGAAACTCAAGAATGCGTTTTAGAAGACGCTCTGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 ATCATAGCTGAAGCTATGGCTAAAGTTGGAAAAGGAGGTGTTATCACAGTTGAGGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCA
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                                                                                                                      <u> AAAGGTCTTGAAACTACATTAGATGTGGTTTGAAGGAATGAAGTTTGACCGTGGCTACCTC</u>
                                                                                                                                                                                                                                      TCTCCATACTTTGTAACTAATCCTGAGAAATGGTTTGTGAACTTGATAACCCTTATATC
                                                                                                                                                                                                                                                                                                                                                   CTTTGTAATGAGAAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTT
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                                                                                                                                                                                                                      Sequence 50, Application US/10267311

Publication No. US20030050469A1

GENERAL INFORMATION:

APPLICANT: Siegel, Marvin

APPLICANT: Mizzen, Lee A.

TITLE REFERENCE: 12071/002001

CURRENT APPLICATION NUMBER: US/10/267,311

CURRENT APPLICATION NUMBER: US/09/613,303

PRIOR FILING DATE: 2002-10-09

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 1999-07-08

NUMBER OF SEQ ID NOS: 55

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 50

LUCKHARE FASTS AND SECOND SE
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Pred. No. 4e-131;
0; Mismatches 532; Indels
    177912 GCCTTAATCGCTGATATCCCAGAAGAGAAA 177883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: fusion sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 65.8%;
Matches 1035; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (1)...(1923)
US-10-267-311-50
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Sequence 13, Application US/09960428

Barent No. US20020115147A1

GRNERAL INFORMATION:
APPLICANT: Roche Diagnostics GmbH

TITLE OF INVERNION: Method for producing an active heterodimeric AMV-RT in prokaryoting File Reference: 5272/00/
CURRENT APPLICATION NUMBER: US/09/960,428

CURRENT APPLICATION NUMBER: 2010-09-21

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.1
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                                                                                               APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
IIILE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
IIILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                41.9%; Score 689.6; DB 9; 65.1%; Pred. No. 4.1e-131;
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0; Mismatches 549;
                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 380
                                        US/09841132
                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Chlamydia pneumoniae
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                                     Sequence 380, Application Patent No. US20020061848A1
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Matches 1035; Conserv
                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                               Score 684.4; DB 10; Length 2155;
Pred. No. 5.3e-130;
0; Mismatches 601; Indels 0;
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Best Local Similarity 63.53
Matches 1045; Conservative
                                                                 TYPE: DNA ORGANISM: Escherichia coli
SEQ ID NO 13
LENGTH: 2155
                                                                                                                                              US-09-960-428-13
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US-10-157-317-26

is Sequence 26, Application US/10157317

publication No. US2003023235A1

centeral inpormation:

APPLICANT: Surber, Mark W.

APPLICANT: Surber, Mark W.

APPLICANT: Surber, Mark W.

APPLICANT: Surber, Mark W.

APPLICANT: Neil Berkley

TITLE OF INVENTION: MINICELL-BASED SCREENING FOR COMPOUNDS

TITLE OF INVENTION: PROTEINS THAT MODULATE THE ACTIVITY OF SIGNALLING

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION: DATE: 2002-05-28

CURRENT FILING DATE: 2002-05-28

PRIOR FILING DATE: 2002-02-25

PRIOR PRIOR FILING DATE: 2002-02-25

PRIOR FILING DATE: 2002-02-25

PRIOR FILING DATE: 2002-02-25

PRIOR FILING DATE: 2002-02-25

PRIOR FILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 257

SOFTWARRE: FastSEQ for Windows Version 4.0

SEQ ID NO 26

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3033 ATCTCTGAAGAGTCGGTATGGAGCTGGAAAAGCAACCCTGGAAGACCTGGGTCAGGCT 3092
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                                               AAACGTGTAGTTATTGACAAAGAAAATACTACTATCGTTGATGGTGCTGGAAAATCAGAA
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US-10-157-339-26
Sequence 26, Application US/10157339
Sequence 26, Application US/10157339
Publication No. US20040005700A1
GENERAL INFORMATION:
APPLICANT: Surber, Mark W.
TITLE OF INVENTION: POROPLASTS
FILE REFERENCE: MPEX. 008D03
CURRENT APPLICATION NUMBER: US/10/157,339
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/293,566
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2002-05-25
PRIOR FILING DATE: 2002-05-25
PRIOR FILING DATE: 2002-05-25
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 257
SOFTWARE: PASSEQ for Windows Version 4.0
SENGTH: 3840
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                                                                                                                                                           Score 684.4; DB 12;
Pred. No. 6.6e-130;
0; Mismatches 601;
                                                                                       OTHER INFORMATION: Fusion protein US-10-157-317-26
                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                           Query Match
41.6%;
Best Local Similarity 63.5%;
Matches 1045; Conservative
  LENGTH: 3840
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                                                                                Length 3840;
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41.6%; Score 684.4; DB 12; Length
Best Local Similarity 63.5%; Pred. No. 6.6e-130;
Matches 1045; Conservative 0; Mismatches 601; Indels
                          ; OTHER INFORMATION: Fusion protein US-10-157-339-26
ORGANISM: Artificial Sequence
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AAACGIGIAGIIATIGACAAAGAAAAIACIACIAICGIIGGIGCIGGAAAAICAGAA 1020
                                                                         AAACGIGITGITGATCAACAAGACACCACCACTATCATCGATGGCGTGGGTGAAGAAGT 3152
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US-10-157-305A-26

Sequence 26, Application US/10157305A

Publication No. US2030166099A1

GENERAL INFORMATION:
APPLICANT: Subbadini, Roger A.
APPLICANT: Subbadini, Roger A.
APPLICANT: Neil Berkley
CHERENCE: MERK W.
APPLICANT: Robert Klepper
TITLE OF INVENTION: MINUEEL: COMPRISING MEMBRANE PROTEINS
FILE REFERENCE: MFEX.008DV1
CURRENT APPLICATION NUMBER: 06/293,566
PRIOR PLILNG DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 60/359,843
PRIOR APPLICATION NUMBER: 00/359,843
PRIOR APPLICATION NUMBER: 10/154,951
PRIOR APPLICATION NUMBER: 2002-05-25

PRIOR APPLICATION NUMBER: 10/154,951
PRIOR PILING DATE: 2002-05-25

PRIOR PILING DATE: 2002-05-25

PRIOR APPLICATION NUMBER: 10/154,951

PRIOR PILING DATE: 2002-05-25

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 26

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APPLICANT: Sabbadini, Roger A.
APPLICANT: Neil Berkley
TITLE OF INVENTION: MINICELL-BASED TRANSFECTION
FILE REFERENCE: MPEX.00BD/10/157,391
CURRENT APPLICATION NUMBER: US/10/157,391
CURRENT FILING DATE: 2002-05-28
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2002-05-28
PRIOR FILING DATE: 2002-05-24
PRIOR FILING DATE: 2002-02-25
PRIOR FILING DATE: 2002-02-25
PRIOR FILING DATE: 2002-02-25
PRIOR FILING DATE: 2002-02-25
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 257
SOFTWARE: FastSEQ for Mindows Version 4.0
SEQ ID NO 26
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Publication No. US20030166279A1
GENERAL INFORMATION:
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                                                                                                       Query Match 41.6%; Score 684.4; DB 13; Best Local Similarity 63.5%; Pred. No. 6.6e-130; Matches 1045; Conservative 0; Mismatches 601;
                                        ; OTHER INFORMATION: Gene encoding a fusion protein US-10-157-305A-26
ORGANISM: Artificial Sequence
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3093 AAACGTGTTGTGATCAACAAAGACACCACCACTATCATCGATGGGGTGAGGAGAAGAGCT 3152
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Sequence 26, Application US/10157096

Sequence 26, Application US/10157096

Sequence 26, Application US/10157096

PUBLication No. US2030190601A1

SERVENCANT: Sabbadini, Roger A.

APPLICANT: Subbadini, Roger A.

TITLE OF INVENTION: TARGET DISPLAY ON MINICELLS

FILE REFRENCE: MERK. 08DV12

CURRENT APPLICATION NUMBER: US/10/157,096

CURRENT FILING DATE: 2002-05-28

PRIOR APPLICATION NUMBER: 60/293,566

PRIOR FILING DATE: 2002-02-25

PRIOR APPLICATION NUMBER: 60/359,843

PRIOR APPLICATION NUMBER: 10/154,51

PRIOR APPLICATION NUMBER: 10/154,51

PRIOR PILING DATE: 2002-05-24

NUMBER: OF SEQ ID NOS: 257

NUMBER: OF SEQ ID NOS: 257
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ORGANISM: Artificial Sequence
PEATURE:
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SEQ ID NO 26
LENGTH: 3840
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                                       ; OTHER INFORMATION: Fusion protein US-10-157-391-26
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Pred. No. 6.6e-130;
0; Mismatches 601;
; OTHER INFORMATION: Fusion protein US-10-157-096-26
                                                                                                                                    Query Match.

Best Local Similarity 63.5%;
Matches 1045; Conservative
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3093 AAACGTGTTGTGATCAACAAAGACACCACTATCATCGATGGCGTGGGTGAAGAAGCT 3152 GATATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTAT 1080 GTTGGAGCTGCTACTGAAACTGAAATGAAAGAGAAGGATCGTGTAGAAGATGCTCTA 1200 1201 AATGCAACAAGAGCTGCGGTTGAAGAAGGTATTGTCCCTGGTGGTGGTACTGCTTTTGTC 1260 GCATCAGGAGAATATGAAGACCTTATTAAAGCTGGTGTCATTGATCCTAAAAAAGTTACA 1500 CGIATTGCATTACAAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGCGCT 1560 cerrerecrecagnacecaerrereresecresecreareareaceaecaeareare 3393 CGCGTAGCGTCTAAACTGGCTGACCTGCGTGGTCAGAACGAAGACCAGAACGTGGGTATC 3452 AATATCATCCGTCGTTCTCTTGAAGAGCCTTTACGTCAAATTGCTGCAAATGCTGGCTAT 1380 3453 AAAGTIGCACIGCGIGCAATGGAAGCICCGCIGCGICAGATCGIAITGAACIGCGGCGAA 3512 3513 GAACCGICIGITGITGCTAACACCGITAAAGGCGGCGACGGCAACTACGGTTACAACGCA 3572 3693 Griacceaccrecceaaaaacearecaecreacrraececerecreceeriarideeceec 3752 3213 GACCGTGAAAAACTGCAGGAACGCGTAGCGAAACTGGCAGGCGCGTTGCAGTTATCAAA GCAATCCAGGGCCGTGTTGCTCAGATCCGTCAGATTGAAGAAGCAACTTCTGACTAC GATCGTGAAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCAT 3273 GTGGGTGCTGCTACCGAAGTTGAAATGAAAAAAAAAAAGGCACGCGTTGAAGATGCCTG 3333 CACGCGACCCGTGCTGCGGTAGAAGACGCGTGGTTGCTGGTGGTGGTGTTGCGGTTGTTG CGCTCCATTAAAGTCCTTGATATTAAACCTGCTGATGATGATGAACTTGCTGGACTT GAAGGTTCTATTGTTGTAGAAAAGTTCGTGAACCAAAAGATGGTTTTGGATTTAATGCT ATTGCTGAAAAACCAGAACCTAAAAAAGATATGCCTATGCCTGGCGGTGGTATGGGTGGT ATGGGTGGTATGGACGGTATGTACTA 1646 Arcecrecarecececarearera 3778

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:

January 29, 2004, 13:07:12 ; Search time 89 Seconds (without alignments) 8168.068 Million cell updates/sec

1 atggcttctaaagaaatcct......gtatggacggtatgtactag 1647 US-09-077-574A-1 1647 Title: Perfect score:

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Searched:

1139956 Total number of hits satisfying chosen parameters:

569978 seqs, 220691566 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued Patents NA:*
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6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			%			SUMMARIES	
Result No.	ult No.	Score	Query Match	Length I	DB	ID	Description
	Н	748.8	45.5	1653	4	US-09-328-352-1382	Sequence 1382, Ap
	7	725.8	44.1	1830121	4	US-09-557-884-1	9 1,
	3	725.8	44.1	1830121	4	US-09-643-990A-1	Sequence 1, Appli
υ	4	690.2	41.9	1230025	4	US-09-198-452A-1	'n
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	15	610.4	7	2284	0	98	28,
	16	610.4	37.1	2284	۳	US-08-432-697-28	28,
	17	2	37.1	2284	m	-80	28,
	18	553.2	3	1656	4	US-09-252-991A-7638	763
υ	19	553.2	3	1722	4	-09-252	7917
	20	480.6	29.5	1050	4	US-09-107-532A-3030	3030,
	21	441.2	26.8	1777	4	US-08-828-199A-1	1, App
υ	22	44	26.7	580073	4	US-08-545-528D-1	1,
	23	439.8	9	2051	4	-09-207-388-	8
	24	439.4	26.7	1647	4	US-09-207-388-9	6
	25	439.4	26.7	1707	4	US-09-207-388-10	10,
	56	427.4		1653	4	-09-207-38	9
	27	427.4	26.0	1713	4	US-09-207-388-7	7,

Sequence 52, Appl	Sequence 3, Appli	Sequence 16, Appl	Sequence 28, Appl	Sequence 20, Appl	3, Aj	Sequence 2, Appli	Sequence 1, Appli	Sequence 10, Appl	Sequence 10, Appl	Sequence 113, App	113,	Sequence 113, App	Sequence 113, App	Sequence 113, App	Sequence 159, App	Sequence 159, App	Sequence 159, App
US-09-613-303-52	US-09-613-303-3	US-09-613-303-16	US-09-613-303-28	US-09-613-303-20	US-08-955-565A-3	US-09-1:03-840A-2	US-09-103-840A-1	US-08-461-775-10	US-09-031-606-10	US-08-997-080-113	US-08-997-362-113	US-09-095-855-113	US-09-324-542-113	US-09-205-426-113	US-08-997-080-159	US-08-997-362-159	US-09-095-855-159
1944 4	1623 4	1920 4	1947 4	2847 4	4380 4	4403765 3	4411529 3	1620 2	1620 3	1569 2	1569 2	1569 3	1569 4	1569 4	1626 2	1626 2	1626 3
25.9	24.7	24.7	24.7	24.7	24.7			24.1	24.1	23.7	23.7	23.7	23.7	23.7	23.7	23.7	23.7
425.8	406.2	406.2	406.2	406.2	406.2	406.2	406.2	396.6	396.6	390.8	390.8	390.8	390.8	390.8	390.8	390.8	390.8
28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 US-09-328-352-1382 Sequence 1382, Application US/09328352 Patent No. 6562958 GENERAL INFORMATION: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: NUMBER: US/09/328,352 TITLE OF INVENTION NUMBER: US/09/328,352 CURRENT FILING DATE: 1999-05-04 CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 8252 EMPTH: 1653 TRPE: DNA CREATISH: 1653 CREATISH: 1653 CREATISH: US/09/328-352-1382	Query Match 45.5%; Score 748.8; DB 4; Length 1653; Best Local Similarity 66.6%; Pred. No. 2.2e-187; Matches 1087; Conservative 0; Mismatches 542; Indels 3; Gaps 1;	OY 1 AIGSCITCTAAAGAAAICCITITIGAIGCITAAAGCCGGIGAAAACTITCACGAGGIGIA 60	Qy 61 GATAAACTTGGAAATGCTGTTAAAGTAACACTTGGACCTAAAGGCCGTAATGTCGTTATT 120	Qy 121 GAAAAGTCTTTTGGTTCCCAGTTATTACAAAAGATGGTGTATCTGTTGCAAAAGAAATT 180	QY 181 GAACTTGAAGATAAGGTTTGAAAATATGGGGCGCTCAAATGGTTAAAGAAGTAGCTCCCGAAA 240	QY 241 ACTAGGGATATIGCTGGTGATGGAACTACAACAGCGACGTCCTTGCACAAGCTATITAT 300	OY 301 CGTGAAGGTGTAAAACTTGTAGCAGCTGGTCGTAATCCTATGGCCATTAAACGTGGCATA 360 119	OY 361 GATAAAGCTGTTGGTGGTGATAAGAACTAAGGGACATTACAAAGCCTACTGGTGAC 420
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1579 ATTACTGACATTCCTGAAGACAAACCAGCT---GCTCCAGATATGGGCGGTATGGGTGT 1635
                                                                                       ATTGCTGAAAAACCAGAACCTAAAAAGATATGCCTATGCCTGGCGGTGGTATGGGTGGT
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REGISTRATION NUMBER: 41,971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
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RESOUR.
US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 65058B1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of
; TITLE OF INVENTION: The Amenophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof
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Pred. No. 7e-180;
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                                                                                                                                                                                                                                                                 ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
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REPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: «Unknown»
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APPLICATION NUMBER: 08/476,102
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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		the Haemophilus inf Thereof, and Uses T CORRESPONDENCES: 1 CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: STREET: Human Genome Sciences, STREET: 9410 Key West Avenue CITY: Rockville, STATE: MD COUNTRY: USA COUNTRY: USA ZIP: 20850 COMPUTER READABLE FORM: MEDIUM TYPER: 3 L/2 inch diskette	CURRENT APPLICATION OF SETAM. SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/643,990A FILING DATE: 23-Aug-2000 CLASSIFICATION: <unimimimimimimimimimimimimimimimimimimim< th=""><th>NAME: Kenley K. Hoover REGISTRATION NUMBER: 40,302 REFERENCE/DOCKET NUMBER: PB186F1C1 TELECHONNINICATION INFORMATION: TELEPHONE: 301-610-5790 TELEFAX: 310-309-8439 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1830121 base pairs</th></unimimimimimimimimimimimimimimimimimimim<>	NAME: Kenley K. Hoover REGISTRATION NUMBER: 40,302 REFERENCE/DOCKET NUMBER: PB186F1C1 TELECHONNINICATION INFORMATION: TELEPHONE: 301-610-5790 TELEFAX: 310-309-8439 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1830121 base pairs
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US-09-198-452A-1/c
; Sequence 1, Application US/09198452A
; Patent No. 6559294
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ORGANISM: Chlamydia pneumoniae
FEATURE:
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OTHER INFORMATION: n=a or c
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LOCATION: (15001)..(30000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            565830 TTAATCTCACAAGCAATGGAAAAAGTGGGCAAGGAAGGTGTAATTACTGTTGAAGATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              541 AAAGGTCTTGAAACTACATTAGATGTGGTTGAAGGAATGAAGTTTGACCGTGGCTACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTCCATACTTTGTAACTAATCCTGAGAAATGGTTTGTGAACTTGATAACCCTTATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTTGTAATGAGAAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            566010 CTrcrigradanaaaaarcrcraacarrcgrdaarracrrccgrgradaaggcgrr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           566070 GCGAAAGCAGGTAAACGTTATTAATCATCGCTGAAGACGTGGAAGGCGAAGCGCTTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACACTTGTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          566130 ACCTTAGTGGTAACACTATGCGCGGTATCGTGAAGTTGCAGCCGTGAAAGCACCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTGGTGAACGCCGTAAAGCTATGCTTGAAGATATTGCTATCCTTACTGGAGGAGAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         901 ATATTIGAAGATCGIGGTATAAAGCTTGAAAATGTAAGCTTGTCTTTTAGGAACAGCT
                                                                                                                                      6; Gaps
                                                                                                      Length 1830121;
                                                                                                                                   Indels
                                                                                                  Score 725.8; DB 4;
Pred. No. 7e-180;
0; Mismatches 557;
                                                    ä
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                    44.1%;
                                                                                                                               Matches 1086; Conservative
                                                                                                                  Local Similarity
                                                               US-09-643-990A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421
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GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preven
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
CURRENT PPILICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                               566310 AAACGTGTTGTTATCAATAAAGATAACACAATTATTGATGGTATCGGCGATGAAGCA 566369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         566909
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AAACGIGIAGITATIGACAAAGAAAAIACIACIAIGGIGAIGGIGCIGGAAAAICAGAA 1020
                                                                                                                                                                                                                                                                                                                                         1140
                                                                                                                                                                                                                           566370 CAAATCAAAGGTCGTGTGTGCTCAAATTCGTCAGCAAATCGAAGAAGAATCAACTTCTGACTAC
                                                                                                                                                                                                                                                                                                                                     GATCGTGAAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCAT
                                                                                                                                                                                                                                                                                                                                                                                     566490 GTGGGCGCAGCAACTTGAAATGAAAGAGAAAAAGATGTGGTGTAGATGCATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             566790 GCAGGAACAGAACAGTACGCCGATATGATCGAATGGGTATCTTAGATCCAACTAAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATGCAACAAGAGCTGCGGTTGAAGAAGAATTGTCCCTGGTGGTGGTACTGCTTTTGTC
                                                                                                                                                                  GATATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTGGAGCTGCTACTGAAACTGAAATGAAAGAGAAGAAGATCGTGTAGAAGATGCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     566550 CATGCAACTCGTGCAGCGGTTGAAGAAGGTATCGTTGCTGGTGGTGGCGTTGCATTAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTAATATCATCCGTCGTTCTTCTTTGAAGAGCCTTTACGTCAAATTGCTGCAAATGCTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1558 GCTATTGCTGAAAAACCAGAACCTAAAAAAGATATGCCTATGCCTGGCGGTGGTATGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCTC---CATTAAAGTCCTTGATGATATTAAACCTGCTGATGATGATGAACTTGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 566610 CGCGCASSAGCGAAAGTTGCAGCAAGCCTAAAAGGTGACAACGAAGAACAAATGTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   566670 ATCAAACTTGCATTACGTGCTATGGAAGCGCCTTTACGTCAAATCGTCACTAACGCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATGAAGGTTCTATTGTAGAAAAAGTTCGTGAACCAAAAGATGGTTTTGGATTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          566730 GAAGAAGCTTCAGTTGTGGCAAGTGCGGTTAAAAATGGCGAAGGAAACTTTGGTTATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTGCATCAGGAGAATATGAAGACCTTATTAAAGCTGGTGTCATTGATCCTAAAAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1498 ACACGTATTGCATTACAAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGC
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NAME/KEY: misc feature
LOCATION: (105001)..(120000)
CTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (12001)..(135000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (135001)..(150000)
CTHER INFORMATION: n=a or c or g or t
CTHER INFORMATION: n=a or c or g or t OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc.feature
LGCATION: (30001)..(4500)
OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc.feature
LCCATION: (45001)..(6000)
OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature
LOCATION: (315001)..(330000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (330001)..(345000)
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JTHER INFORMATION: n=a or c or g or t AAME/KEY: misc feature
LOCATION: (21001)..(225000)
THER INFORMATION: n=a or c or g or t
AAME/KEY: misc feature
COCATION: (225001)..(240000)
THER INFORMATION: n=a or c or g or t NAME/KEY: misc feature OCATION: (240001)..(255000) OTHER INFORMATION: n=a or c or g or t WAME/KEY: misc feature LOCATION: (255001)..(270000) NTHER INFORMATION: n=a or c or g or t AME/KEY: misc feature LOCATION: (28501)..(300000) THER INFORMATION: n=a or c or g or t LOCATION: (75001)..(90000) OTHER INFORMATION: n=a or c or g or t OCATION: (180001). (195000)
THER INFORMATION: n=a or c or g or t OCATION: (30001)..(315000)
THER INFORMATION: n=a or c or g or t NAME/KEY: misc_feature LOCATION: (360001)..(375000) DIHER INFORMATION: n=a or c or g or NAME/KEY: misc feature LOCATION: (60001)..(75000) OTHER INFORMATION: n=a or c or g or AME/KEY: misc feature OCATION: (195001)..(210000) THER INFORMATION: n=a or c or g or VAME/KEY: misc feature LOCAȚION: (27001)..(285000) JTHER INFORMATION: n=a or c or LOCATION: (90001)..(105000) OTHER INFORMATION: n=a or c or NAME/KEY: misc feature LOCATION: (75001)..(900 NAME/KEY: misc feature COCATION: (90001)..(105 IAME/KEY: misc feature NAME/KEY: misc_feature

NAME/KEY: misc feature
LOCATION: (54001)..(555000)
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LOCATION: (55501)..(570000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (570001)..(585000)
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LOCATION: (450001)..(465000)
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NAME/KEY: misc feature
LOCATION: (46501)..(480000)
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NAME/KEY: misc feature
LOCATION: (480001)..(495000)
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (420001)..(43500)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc feature OCATION: (630001)..(645000) THER INFORMATION: n=a or c or JOCATION: (52501)..(540000) NAME/KEY: misc_feature LCCATION: (70501)..(720000) OTHER INFORMATION: n=a or c or NAME/KEY: misc_feature AME/KEY: misc feature AME/KEY: misc_feature NAME/KEY: misc_feature

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178333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178872 recageractreceaeaarecagaaerecaagarecerriragaagaegeerergar 178813
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                                                                                                                                                                                                                                                                                                                                                                                           178752 GCAGAATCTGGACGCCCTCTTTTAATCATTGCAGAAGAAATTGAAGGAGAAGCTTTAGCA 178693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           961 AAACGIGIAGITAITGACAAAGAAAATACTACTATCGITGAIGGIGCIGGAAAAICAGAA 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1081 GATCGTGAAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCAT 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178692 ACTCTAGTAGTCAATAGACTCCGTGCATTCAGAGTCTGTGCAGTGAAAGCTCCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178632 ITCGGTGACAGAAGAAAAGCTATGTTAGAAGACTATCGCTATCCTTACTGGTGGCCAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178392 GACAAAGAAAAACTCCAAGAGGGTTTAGCTAAACTCTCCGGTGGTGTCGCCGTAATCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178212 CGCTGTATCCCTACACTAGAAGCTTTCCTTCCTATGCTAGCAAACGAAGACGAAGCTATT
                           541 AAAGGTCTTGAAACTACATTAGATGTGGTTGAAGGAATGAAGTTTGACCGTGGCTACCTC
                                                                         178932 AAAGGCTTCGAAACTGTTCTCGACGTTGTAGAAGGAATGAACTTCAACCGTGGATACCTC
                                                                                                                                                                                                                                   661 CTTTGTAATGAGAAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                841 TTTGGTGAACGCCGTAAAGCTATGCTTGAAGATATTGCTATCCTTACTGGAGGAGGAGAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178572 GTTAGCGAAGAACTTGGCATGAAACTAGAGAATACAACTCTAGCAATGTTAGGAAAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1021 GATATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178332 GTAGGAGCTGCTACCGAAATAGAGATGAAAGAGAAAAAAGACAGAGTAGATGATGCACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1261 CGCTCCATTAAAGTCCTTGATGATATTAAACCT-----GCTGATGATGATGAACTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178092 GGTAAAGAAGGCGCTATCATTTGTCAAGGTTCTAGCAAGATCTGCAAATGAAGGCTAT
                                                                                                                               TCTCCATACTTTGTAACTAATCCTGAGAAAATGGTTTGTGAACTTGATAACCCTTATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       901 ATATTTGAAGATCGTGGTATAAAGCTTGAAAATGTAAGCTTGTCTTCTTTAGGAACAGCT
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; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
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                                                                                                                                                                                                                                                                                                                                                                                        Length 1926;
                                                                                                 APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                      Score 689.8; DB 4;
Pred. No. 7.7e-172;
0; Mismatches 532;
                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                            : 2000-07-10
JMBER: US 60/143,757
1999-07-08
                          Sequence 50, Application US/09613303
Patent No. 6495347
                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: fusion sequence NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 65.8%;
Matches 1035; Conservative (
                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                    APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1)...(1923)
US-09-613-303-50
                                                         GENERAL INFORMATION:
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SEQ ID NO 50
LENGTH: 1926
RESULT 5
US-09-613-303-50
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                                                                                                        668 ATGAGAAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTTGCTAAAG 727
602 ACATGGTGACAGATAGCGAAAAATGGTGGCTGACCTTGAAAATCCGTACATTTTGATTA 661
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1655 TCTATCGTTATCGATCGTTTGAAAAATGCTGAGCTTGGTATAGGATTTAACGCAGCAACT 1714
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TCTGAAGCAATGGAAAAAGTTGGCAAAGACGGTGTCATCACCATCGAAGAGTCACGTGGT
                                                                                                           818 ATGGAAACAGAGCTTGAAGTCGTAGAAGGAATGCAGTTTGACCGTGGTTACCTTTCACAG
                                                                                                                                                        TACTTTGTAACTAATCCTGAGAAAATGGTTTGTGAACTTGATAACCCTTATATCCTTTGT
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    INVENTION: Streptococcus pneumoniae Polynucleotides and
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0; Mismatches 534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 687.6;
                                                                                                                                                                                                                E: Diskette, 3.50 inch, 1.
HP Vectra 486/33
SYSTEM: MSDOS version 6.2
                                                                   Sciences,
                                                                                                                                                                                                                                                                                                                              US/08/961,527
                                                     SSEE: Human Genome Scie.
19410 Key West Avenue
Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.7%;
65.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5365 base pairs
                                                                                                                                                                                                                                                                             SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                        NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                      ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                             OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
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Matches 1034; Conserv
                                                                                                                                    Maryland
                                                                 ADDRESSEE:
STREET: 941
CITY: Rocky
STATE: Mary
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Patent No. 6197547
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US-09-472-971-7
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                                                                     Sequence 5, Application US/09472971
Patent No. 6197547
GENERAL INFORMATION:
APPLICANT: SOGO, Kazuyo
APPLICANT: YANAGI, Hideki
APPLICANT: YUKA, Takashi
TITLE OF INVENTION:
FILE REFERENCE: 1422-409P
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 41.5%; Score 682.8; DB 3; Best Local Similarity 63.4%; Pred. No. 5e-170; Matches 1044; Conservative 0; Mismatches 602;
                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/472,971
CURRENT FILING DATE: 1999-12-28
EARLIER APPLICATION NUMBER: JP10-372965
EARLIER FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 7
1835 AATAAACCAGAACC 1848
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SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Escherichia coli
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                                           RESULT 7
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ACACTIGIAGICAATAAGCICCGIGGAGCACTCCAAGITGIAGCCGTAAAAAGCICCTGGI
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Patent No. 6077706
GENERAL INFORMATION:
APPLICANT: Covacci, Antonello
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Telford, John
Macchia, Giovanni
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   APPLICANT: SOGO, Kazuyo
APPLICANT: YANAGI, Hideki
APPLICANT: YURA, Takashi
TITLE OF INVENTION: TRIGGER FACTOR EXPRESSION PLASMIDS
FILE REPERENCE: 1422-409P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 602;
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Pred. No. 8.1e-170;
                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/472,971
CURRENT FILING DATE: 1999-12-28
EARLIER APPLICATION NUMBER: UPIO-372965
EARLIER FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 Argeriecesecsarieseaecaecaecaeceaecerecraserrarasearrirraaasaas 361
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                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.25
     for Vaccines and Diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 2.2e-159;
0; Mismatches 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,848
FILING DATE: 21-0CT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0316.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,260
                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                Chiron Corporation
                                                                                                           4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA (genomic)
                                                                                                                                                                                                                                                                 Floppy disk
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Best Local Similarity 62.9
Matches 1032; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: singl
TOPOLOGY: linear
                                                                                                                                                              California
                             NUMBER OF SEQUENCES:
                                                                                                                                Emeryville
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                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                      COUNTRY:
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    502 TTGAAGATGAATTGGATGTCGTAGAAGGCATGCAATTTGATAGAGGCTACCTCTCCCCTT 661
                                                                                                                                                                        722 CGGATAAAAAATCTCTAGCATGAAAGACATTCTCCCGCTACTAGAAAAAACCATGAAAAG
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                                                 608 ACTITGIAACIAAICCIGAGAAAIGGIIIGIGAACIIGAIAACCCIIAIAIAICCIIIIGIA
                                                                                         ATTITIGIAACGAACGCTCAGAAATGACCGCTCAATTGGATAATGCTTACATCCTTTAA
                                                                                                                                      668 ATGAGAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTTGCTAAAG
                                                                                                                                                                                                                         TAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCAACACTTG
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                                                                                                                                                                                                                                                                                                            TAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGTTTTGGTG
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                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Covacci, Antonello
APPLICANT: Bugnoll, Massimo
APPLICANT: Bugnoll, Massimo
APPLICANT: Telford, John
APPLICANT: Rappuoli, Rino
TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And
TITLE OF INVENTION: Diagnostics
FILE REFERENCE: CHIR0044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 GCTATGGCGCTCCAAGCATCACCAAGACGCGTGAGCGTGGCCTAAAGAGATTGAATTAA
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Pred. No. 2.2e-159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/08/471,491B
CURRENT FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
                                                                                                         1676 GAGGCATGGGCGCATGATGTA 1697
                                                                                                                                                                                                                     Sequence 7, Application US/08471491B
Patent No. 6090611
                                                                 GTGGTATGGACGGTATGTACTA
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Best Local Similarity 62.9%;
Matches 1032; Conservative
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Sequence 6, Application US/08256847C Patent No. 6403099
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                                                                                      APPLICANT: Bugnoli, Massimo
APPLICANT: Telford, John
APPLICANT: Telford, John
APPLICANT: Rappuoli, Rino
TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And
TITLE OF INVENTION: Jagnostics
FILE REFERENCE: CHIRO057
CURRENT APPLICATION NUMBER: US/08/466,662B
NUMBER OF SEQ ID NOS: 1995-06-06
NUMBER OF SEQ ID NOS: 2.1
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                              Sequence 7, Application US/08466662B
Patent No. 6130059
GENERAL INFORMATION:
APPLICANT: COVACCI, Antonello
                                                                                                                                                                                                                                                                                                        ORGANISM: Helicobacter pylori
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                   US-08-466-662-7
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US-09-134-001C-1868; Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
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                                                  APPLICANT: Correnting Page 11, Francesco TTILE OF INVENTION: Conjugates Formed From Heat Shock Proteins And Oligo or Polysacch FILE REPRENCES: CHRR-0042
CURRENT APPLICATION NUMBER: US/08/256,847C
CURRENT RILING DATE: 1994-11-01
PRIOR APPLICATION NUMBER: PSTAPES PRIOR PRICATION NUMBER: PSTAPES PRIOR PRICATION NUMBER: P192A00058
PRIOR FILING DATE: 1992-03-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Version 3.1
SEQ ID NO 6
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Pred. No. 2.2e-159;
0; Mismatches 601;
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ilarity 62.9%;
Conservative
                                              APPLICANT: Rappuoli, Rino APPLICANT: Costantino, Pa
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FEATURE:
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                     TAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAAGCTCCTGGTTTTTGGTG
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US-09-221-017B-895/c
; Sequence 895, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TILLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
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STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
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COMPUTER READABLE FORM:
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE POF INVENTION: DEPERMINES FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
NUMBER OF SEQ ID NOS: 5674

NUMBER OF SEQ ID NOS: 5674

FENDAMENT: 1673
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Pred. No. 9e-159;
                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                 38.9%;
63.1%;
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 38.9
Best Local Similarity 63.1
Matches 1020; Conservative
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                                                                                                                                              FastSEQ for Windows Version 2.0b
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                                                                                                                                                                                                                     UMBER: US/09/221,017B
23-DEC-1998
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REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
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INFORMATION FOR SEQ ID NO: 895:
SEQUENCE CHARACTERISTICS:
LENGTH: 2416 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
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SYSTEM: Windows
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Best Local Similarity 62.0
Matches 1009; Conservative
                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              650-494-0792
                      Diskette
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FILING DATE: 23-DE
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                                                              COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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ORIGINAL SOURCE
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US-09-221-017B-895
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                                                      CTAAAGAAATCCTTTTTGATGCTAAAGCCCGTGAAAACTTTCACGAGGTGTAGATAAAC 67
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Ferrero, Richard L.
Thiberge, Jean-Michel
VVENTION: IMMUNOSENIC COMPOSITIONS AGAINST
VVENTION: HELLCOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
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                                                                                                                                                                                   CTGAAAAACCAGAACCTAAAAAGATATGCCTATGCCTGGCGGTGGTATGGTGTATGG 1624
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484 CGGATGTTTTCGAAAACCTCTACACTACCGGTGTTATCGACCCGGCCAAAGTAACACGTG 425
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Dunner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
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SYSTEM: PC-DOS/MS-DOS
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Patent No. 5843460
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TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
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CLASSIFICATION: 435
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TITLE OF INVENTION: IMMI
TITLE OF INVENTION: COM
TITLE OF INVENTION: COM
TITLE OF INVENTION: POL
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5843460
GENERAL INFORMATION:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2061 AAATCAAAGAAAAAAGGGCCCCAGCAATGCCTGATATGGGTGGCATGGGGGGAATGG 2120
                    1148 CTGCTACTGAAACTGAAATGAAAGAAGAAGAAGGATCGTGTAGAAGATGCTCTAAATGCAA 1207
                                                                                         1208 CAAGAGCIGCGGIIGAAGAAGGIAIIGICCCIGGIGGIAGIACIGCIITITGICCGCICCA 1267
1088 AAAAACITCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCATGTTGGAG 1147
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Search completed: January 29, 2004, 15:27:33 Job time : 105 secs bordetella coxiella bu xanthomonas

P48210

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of 7 subunits (By similarity).
-:- SUBCELLULAR LOCATION: Octoplasmic (By similarity).
-:- SIMILARITY: Belongs to the chaperonin (HSP60) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salanoubat M., Genin S., Arriguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Fenard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.,
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation update)
60 kDa chaperonin (Protein Cpn60) (groEL protein)
GROL OR GROEL OR MOPA OR RSC0642 OR RS01546.
Ralstonia solanacearum (Pseudomonas solanacearum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               547 AA.
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CH60_NEIMA
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MEDLINE=21681879; PubMed=11823852;
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-MODEL=Frame+.n5P.model -DEV=xlp
-Q=Cqn2_1/USFTO_spool_p/US09077574/runat_28012004_125846_11606/app_query.fasta_1.1799
-Q=Cqn2_1/USFTO_spool_p/US09077574/runat_28012004_125846_11606/app_query.fasta_1.1799
-DB=SwissProt_41 -QPMT=Fastan -SUFFIX=rsp -MINNATCH=0.1 -LOOPCH=0 -LOOPEXT=0
-DG=SwissProt_41 -QPMT=Fastan -SUFFIX=rsp -MINNATCH=0.1 -LOOPCH=0 -LIST=45
-DGALIGN=120 -THR SCORE=pct -THR MARX.Exl00 -TRR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPWN=pto -NORM=ext -HEAPSIZE=500 -MINLEND -MAXLEND=2000000000
-USER=US09077574_@CGN_1 1_18 @runat_28012004_125846_11606 -NCPU=6 -ICPU=3
-NO MARP -LARCEGUERY -MASN TIMBOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Result No.

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P35861 bradyrhizob P35470 rhizobium m P57006 neisseria m Q8yb53 brucella me

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Q98ax9

Q983s4 rhizobium

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rhizobium

Q91691 P77829 P20110 033500

paracoccus chlorobium rhizobium

Q92462 Q8kf02 Q98ih9 P30718 P25967

Sequence:

Run on:

Searched:

Minimum

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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
60 kDa chaperonin (Protein Cpn60) (groEL protein).
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                            J. Biosci. Bioeng. 94:140-147(2002).
-!- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress
                                                                                                                                                                                                                                         conditions (By similarity).
SUBUNIT: Oligomer of 14 subunits composed of two stacked rings 7 subunits (By similarity).
                         STRAIN=IFO 3283;
Okamoto-Kainuma A., Yan W., Kadono S., Tayama K., Koizumi Y.,
                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to the chaperonin (HSP60) family.
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Pfam; PF00118; cpn60 TCP1; 1.

PROSITE; PS00296; CHAPERONINS_CPN60; 1.

Chaperone; ATP-binding.

SEQUENCE 546 AA; 58106 MW; 3E476AF42F2CD5CC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATAAACTTGCAAATGCTGTTAAAGTAACACTTGGACCTAAAAGGCCGTAATGTCGTTATT 120
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|MetAlaAlaLysAspValValPheGlyAspSerAlaArgSerLysMetValGluGlyVal
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                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions (By similarity).
-!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zysk G., Splettstoesser W.D., Neubauer H.; "Nucleotide sequence comparison of the groE operon of Burkholderia
                                                                                                                                                                                                  Bacteria, Proteôbacteria, Betaproteobacteria, Burkholderiales;
Burkholderiaceae, Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                          7 subunits (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
                                                                                                                                                                                                                                                                                                                        Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00296; CHAPERONINS_CPN60; 1.
Chaperone; ATP-binding.
SEQUENCE 546 AA; 56980 MW; 174B9934345E7315 CRC64;
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374
75
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3
                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
60 kDa chaperonin (Protein Cpn60) (groEL protein)
GROL OR GROEL OR MOPA.

Burkholderia cepacia (Pseudomonas cepacia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
                                                                                              546 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (Soor send an email to license@isb-sib.ch).
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InterPro; IPR001844; Chaprnin Cpn60.
InterPro; IPR002423; Cpn60/TCP-1.
Ffam; PF00118; Cpn60 TCP1; 1.
PRINTS; PR00298; CHAPERONIN60.
PRINTS; PR00394; TCOMPLEXTOP1.
                1618 GGTATGGGTGGTATGGAC 1635
                                         GlyMetGlyGlyMetAsp 545
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                                                                                                                                                                                                                                                                     STRAIN=NCTC 10744;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Best Local Similarity:
                                                                                                                                                                                                                               NCBI_TaxID=292;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTAAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCA 780
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                                                                                                                                    ACTAGCGATATTGCTGGTGATGGAACTACAACAGCAACAGTCCTTGCACAAGCTATTTAT 300
                                                                                                                                                                                                                                      CGTGAAGGTGTAAAACTTGTAGCAGCTGGTCGTAATCCTATGGCCATTAAACGTGGCATA 360
                                                                                                                                                                                                                                                                                                                               GATAAAĞCTGTTGTTGCTGTTACTAAAGAACTAAGCGACATTACAAAGCCTACTCGTGAC 420
GluArgSerPheGlyGlyProThrValThrLysAspGlyValSerValAlaLysGluIle 60
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                                                                         541 AAAGGTCTTGAAACTACATTAGATGTGGTTGAAGGAATGAAGTTTGACCGTGGCTACCTC
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                                                                                                           1321 AATATCATCCGTCGTTCTCTTGAAGAGCCTTTACGTCAAATTGCTGCAAATGCTGGCTAT 1380
                                                                                                                                                                                                                GAAGGTTCTATTGTTGTAGAAAAGTTCGTGAACCAAAAGATGGTTTTGGATTTAATGCT 1440
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CGCTCCATTAAAGTCCTTGATGATATTAAACCTGCTGATGATGATGAACTTGCTGGACTT 1320
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                                                                                                                                                           441 LysileValLeuArgAlaMetGluGluProLeuArgGlnileValThrAsnGlyGlu
                                                                                                                                                                                                                                                        461 GlüAlaServalValValValAlaAlaValAlaAlaGlyLvSGlyAsnTyrGlyTyrAsnAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WOO P.C.Y., Leung P.K.L.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions (By similarity).

-!- SUBBUIT: Oligomer of 14 subunits composed of two stacked rings of 7 subunits (By similarity).

-!- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).

-!- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GROL OR GROEL OR MODA.
Burkholderia pseudomallei (Pseudomonas pseudomallei)
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16-0CT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
60 kDa chaperonin (Protein Cpn60) (groEL protein).
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PROSTITE; PS00226; CHAPERONINS_CPN60; 1.
Chaperone; ATP-binding.
SEQUENCE 546 AA; 57145 WW; E9E9366E
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InterPro; IPR001984; Chaprnin Cpn60.

InterPro; IPR002423; Cpn60/TCP-1.

Pfam; PF00118; cpn60 TCP1; 1.

PRINTS; PR00298; CHAPERONINGO.
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Burkholderiaceae; Burkholderia.
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HSSP; P06139; 1GRL.
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submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Prevents misfolding and promotes the refolding and
- proper assembly of unfolded polypeptides generated under stress conditions (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zysk G., Splettstoesser W.D., Neubauer H.; "Nucleotide sequence comparison of the groß operon of Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last amortation update)
60 kBa chaperonin (Protein Cpn60) (großL protein)
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Burkholderia vietnamiensis.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Oligomer of 14 subunits composed of two stacked rings
                     7 subunits (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the chaperonin (HSP60) family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     546
373
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE, PS00296; CHAPERONINS_CPN60; 1.
Chaperone; ATP-binding.
SEQUENCE 546 AA; 57010 MW; 47FA89399
                                                                                                                                                                                                                                                                                                       HAMAP; MF 00600; -; 1.
InterPro; IPR001844; Chaprnin Cpu InterPro; IPR002423; Cpn60/TCP-1.
Efam; PF00118; cpn60 TCP1; 1.
PRINTS; PR00298; CHAPERONINGO.
PRINTS; PR00304; TCOMPLEXTCP1.
                                                                                                                                                                                                                                                                  EMBL; AF104908; AAC79089.1; -. HSSP; P06139; 1GRL.
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1868.50
81.90%
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62.95%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GITGGAGCTGCTACTGAAACTGAAATGAAAGAGAAGAAGATCGTGTAGAAGATGCTCTA 1200
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LysSerLeuAlaAspGluLeuAspValValGluGlyMetGlnPheAspArgGlyTyrLeu 200
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521 ValAlaGluLeu-----ProLysGluAspAlaProMetProGlyGlyMetProGlyGly 538
                           TCTCCATACTTTGTAACTAATCCTGAGAAAATGGTTTGTGAACTTTGATAACCCTTATATC
                                                                                                                                   GCTAAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCA
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                                                                                              401 HisAlaThrArgAlaAlaValGluGluGlyIleValAlaGlyGlyGlyValAlaLeulle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions (By similarity).
SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGGCTTCTAAAGAAATCCTTTTTGATGCTAAAGCCCGTGAAAAACTTTCACGAGGTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Xiao M., Zheng P., Chen Y.Y.; Xiao M., Zhu C.R., Qian X.M., Zheng P., Chen Y.Y.; "Cloning and Sequencing of the grobSL Operon of Rhodopseudomonas
                                                                                                                                                                                                                                       Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Rhodopseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 subunits (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the chaperonin (HSP60) family.
                                                                                                                                                                                                                                                                                                                                                                                                                            palustris.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP, MF 00600; -; 1.

InterPro; IPR001844; Chaprnin Cpn60.

InterPro; IPR00243; Cpn60/TCP-1.

Pfan, PF00118; cpn60 TCP1; 1.

PRINTS; PR00299; CHAPERONIN60.

PRINTS; PR00296; TCMPLEXTCP1.

PROSITE; PS00296; CHAPERONINS_CPN60; 1.

Chaperone; ATP-binding.

SEQUENCE 546 AA; 57937 MW; 163C7115D68FFFF9 CRC64;
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374
75
95
                                         Q93MH1;
28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
60 kDa chaperonin (Protein Cpn60) (groEL protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
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Matches:
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                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF406639; AAK94943.1; -.
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1868.00
81.93%
68.25%
62.94%
                                                                                                                                                                                                                 Rhodopseudomonas palustris
                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                            NCBI_TaxID=1076;
                                                                                                                                                                                  GROL OR GRÖEL
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                           CH60 RHOPA
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CH60_RHOPA
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Db 441 ThrIleValArgArgAlaLeuGluAlaProLeuArgGlnIleAlaGlnAsnAlaGlyVal 460 381 GAAGGTTCTATTGTTGAAAAAGTTCGTGAACCAAAAGATGGTTTTGGATTTAAT 1437 382 GAAGGTTCTATTGTTGAAAAAGTTCGTGAACCAAAAGATGGTTTTGGATTTAAT 1437 461 AspGlySerValValAlaGlyLysValArgGluSerAspAspLysAlaPheGlyPheAsn 480 0y 1438 GCTGCATCGGAAATAGAAGACTTATTAAAGCTGGTGTCATTGATCCTAAAAAGTT 1497 1498 ACACGTATTGCATTACAAAATGCAACACACAGGTGTCATTGATCCTAAAAAGTT 1497 1498 ACACGTATTGCATTACAAAATGCACATCAGTAGCTGTGTTCTAACTACAGAATGC 1557 0y 1558 GCTATTGCTGAAAAAACCAGAACATGATGCCTGTTGCTTCTAACTACAGAATGC 1557 0y 1558 GCTATTGCTGAAAAAACCAGAACCTAAAAAAGATATGCCTGTTGCTGGCGGTGGTATGGCTT 1617 0y 1558 GCTATTGCTGAAAAAACCAGAACCTAAAAAAGATATGCCTGCGCGGTGGTATGGCT 1617 0y 1558 GCTATTGCTGAAAAAACCAGAACCTAAAAAAAAAAAAAA	RESULT 7 CH60 BURTH ID CH60 BURTH STANDARD; PRT; 546 AA. AC P58723; DT 28-FEB-2003 (Rel. 41, Created) DT 28-FEB-2003 (Rel. 41, Last sequence update) DT 28-FEB-2003 (Rel. 41, Last annotation update) ON GROUP CROWER CROWN (Protein Cpn60) (groEL protein). ON Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; ON NOEL TaxID=57975; RN (I) RP SEQUENCE FROM N.A.	-	. # _ 0 2	ign ed. ore
241 ACTAGCGATATTGCTGGTGATGGAACTACAACAGCAACGTCCTTGCACAGGTATTTAT 300 81 ThrasnaspGlualaGlyAspGlyThrThrThralaThrValLeuAlaGlualaIIelle 100 81 CGTGAAGGTGAAACTTGTAGCAGCTGGTCGTATCTATGGCCATTAAACGTGGCATA 360 81 IJSGLUGIJYLeuLySAlaValalaAlaGlyMetAanbroMetAspLeuLySArgGlyIle 120 81 GATAAAGCTGTTGTTGCTGTTAAAGACTAAAGCGACATTAAAGCGACATTAAAGGCATA 360 81 GATAAAGCTGTTGTTGTTGTTAAAGACTAAAGACGATTAAAGCGACTTACAAAGCTACTGTGAC 420 81 ASpLeuAlaThrAlaLySValValGluSerIleLySAlaAlaSerArgBroValAsnAsp 140 821 CAAAAAAAAAAAAAGTTGGAAACTTGAAACTGTAACAAAGCGTAAT 480 8481 ATCATAGCTGAAACTTGGAAACTTGAAAAGGAGTGTTATCACAGTTGAGGAAGT 540 8481 ATCATAGCTGAAAGTTGGAAAAGGAGGAGTGTTATCACAGTTGAGGAAGCT 540 8481 ATCATAGCTGAAACTTGGAAAAGTTGGAAAAGGAGGTGTTATCACAGTTGAGGAAGCT 540 8481 ATCATAGCTGAAACTTGGAAAAGGAGAGTGTTATCACAGTTGAGGAAGCT 540 8541 AAAGGTCTTGAAACTTAGATGTGAAAAGGAGAGTTATTAGACGTTGAGGAAGCT 600 8541 AAAGGTCTTGAAACTTAGATGTGAAAGGAGAGTGTTATCACAGTTGAGGAAAGCT 600 8541 AAAGGTCTTGAAACTAAGATGAGAAAGGAGAGTGTTATCACAGTTGAGGAAGCT 600 8541 AAAGGTCTTGAAACTTAGATGTGAAAAGGAGAGTGTTATCACAGTTGAGGAAGCT 600 8541 AAAGGTCTTGAAACTTAGATGTGAAAAGGAGAGTGTTATAGACTTAGACGAAGCTC 600 8541 AAAGGTCTTGAAACTTAGATGTGAAAAGAGAAGTAGAGTTATAGATTAGATAAGATAAGATAAGATAAGATAAGATAAGATAAGATAAGAAAAGAAG	TCTCCATACTTTGTAACTAATCCTGAGAAAATGGTTTGTGAACTTGATAACCCTTATATT	261 ThrLeuvalvalAsnLysLeuArgGlyGlyLeuLysIleAlaAlaValLysAlaFroGly 280 841 TTTGGTGAACGCGTAAAGCTATGAAATATTGCTATCCTTACTGGAGGAGAAGCA 900 841 TTTGGTGAACGCGTAAAGCTTGAAAATTGCTATCCTTACTGGAGGAGAAGCA 900 281 PheGlyAspArgArgLysAlaMetLeuGlnAspIleAlaIleLeuThTGlyGlyGlnVal 300 901 ATATTTGAAGATCGTGGTATAAAGCTTGAAAATGTAAGCTTGTCTTTTAGGAACAGCT 960 901 ATATTTGAAGATCGTGGTATAAAGCTTGAAAATGTAAAGCTTGTCTTTTTGGAACAGAGAAAAAAAA	1021 GATATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTAT 1080 ::: :::	1201 AATGCAACAACAACAGCGGTTCAACAACTATTGTCCCTGGTGGTGGTACTGCTTTTTGTC 1260

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STRAIN-ATCC 49882 / Houston 1;
MEDLINE-97419519; PubMed-9274034;
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Salvendla henselae (Rochalimaea Bartonella henselae (Rochalimaea OC Bartonella henselae (Rochalimaea OC Bartonella Proteobacteria; Alphapr CN NCBI_TAXID=38323;

RN (1)

RX SEQUENCE FROM N.A.

RC STRAIN=ATC 49882 / Houston 1;

RX Haake D.A., Summers T.A., McCoy PR Harbard Shock response and groel segment RT Scoulation of intraspecies genet RT Evock protein (groel) gene of Bar
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STRAIN=ATCC 49882 / Houston 1;
Marston E.L., Summer J.W., Repenty R.L.;
"Evaluation of intraspecies genetic variation within the 60 kDa heat shock protein (groEL) gene of Bartonella species: a new phylogenetic
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bartonellaceae; Bartonella.
NCNE_TaxID=38323;
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-FEB-2003 (Rel. 41, Last annotation update)
-KDa chaperonin (Protein Cpn60) (groEL protein)
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                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                Summer J.W., Nicholson W.L., Massung R.F.,
Summer J.W., Nicholson W.L., Massung R.F.,
"PCR amplification and comparison of nucleotide sequences from the
groESL heat shock operon of Ehrlichia species.";
J. Clin. Microbiol. 35:2087-2092(1997).
-!- FUNCTION: Prevents misfolding and promotes the refolding and
proper assembly of unfolded polypeptides generated under stress
conditions (By similarity).
-!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGGCTTCTAAAGAAATCCTTTTTGATGCTAAAGCCCGTGAAAAACTTTCACGAGGTGTA
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                                                                                                                                                                                               7 subunits (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
analysis tool.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
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385
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InterPro; IPR001844; Chaprnin Cpn60.
InterPro; IPR001844; Chaprnin Cpn60.
InterPro; IPR002423; Cpn60/TCP-1.
Pfan; PF00118; Cpn60 TCP1; 1.
PRINTS; PR00298; CHAPERONINGO.
PRINTS; PS00296; CHAPERONINS_CPN60; 1.
PROSITE; PS00296; CHAPERONINS_CPN60; 1.
Chaperone; ATT-binding; Heat shock.
SEQUENCE 547 AA; 57625 MM; EDE25D566D5
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                                                      STRAIN=ATCC 49882 / Houston 1;
MEDLINE=97373904; PubMed=9230387;
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1867.50
81.24*
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62.92*
                                         SEQUENCE OF 1-408 FROM N.A.
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HSSP; P06139; 1GRL.
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Query Match:
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1321 AATATCATCCGTCGTTCTCTTGAAGAGCCTTTACGTCAAATTGCTGCAAATGCTGGCTAT 1380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  961 AAACGIGIAGITATIGACAAAGAAAIACIACIAIGGIGGIGGIGCIGGAAAAICAGAA 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    460 GluAlaAlaIleIleValGlyLySValLeuGluAsnAsnAlaAspThrPheGlyTyrAsn 479
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                                                                                                                                            GATAAAGCTGTTGTTGCTGTTACTAAAGAACTAAGCGACATTACAAAGCCTACTCGTGAC 420
                                                                                                                                                                                                                                                        GCTAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCA
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                                                                                                        421 CAAAAAGAAATAGCTCAAGTTGGAACCATTTCTGCAAACTCTGATACAACAATAGGTAAT
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1557
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1438 GCTGCATCAGGAGAATATGAAGACCTTATTAAAGCTGGTGTCTCATTGATCCTAAAAAGTT 1497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                             500 ValArgSerAlaLeuGlnAsnAlaAlaSerIleAlaSerLeuLeuIleThrThrGluAla
                         480 ThralaThrGlyGluPheGlyAspLeuIleAlaLeuGlyIleValAspProValLysVal
                                                                           1498 ACACGTATTGCATTACAAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGC
                                                                                                                                                       1558 GCTATTGCTGAAAAACCAGAACCTAAAAAAGATATG------CCTATGCCTGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proper assembly of unfolded polypeptides generated under stress conditions (By similarity).
SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rusanganwa E., Gupta R.S.;
"Cloning and characterization of multiple groEL chaperonin-encoding
genes in Rhizoblum meliloti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Becker A., Boutry M., Cadieu B., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portectelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.", Proc. Natl. Acad. Sci. U.S.A. 99:9977-9882 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Sinorhizobium/Ensifer group, Sinorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
30-MAX-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
60 kDa chaperonin | (Protein Cpn60 1) (groEL protein 1).
GROLI OR GROELI OR GROEL-A OR R00792 OR SMC0913.
Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases,
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SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
INDUCTION: By heat shock.
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121 AspLeuAlaValAlaGluValValLysAspLeuLeuAlaLysAlaLysLaLysIleAsnThr 140
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4CEF358957E1B45A CRC64;
            PIR; JN0509; JN0509.

HSSP; P06139; IGRL.

HAMAP; MF 00600; -; 1.

InterPro; IPR001844; Chaprnin Cpn60.

InterPro; IPR002423; Cpn60/TCP-1.

PEAM; PF00118; cpn60 TCP1; 1.

PRINTS; PR00304; TCOMPLEXTCP1.

PROSITE; P800304; TCOMPLEXTCP1.

PROSITE; P800304; CHAPERONINS CPN60; 1.

Chaperone; ATP-binding; Heat Shock; Multigene family;
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  GCTAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCA
                                                                                   ACACTTGTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGT
                                                                                                                                                                    TTTGGTGAACGCCGTAAAGCTATGCTTGAAGATATTGCTATCCTTACTGGAGGAGAAGCA
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01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
66 kba chapperonin (Protein Cpn60) (groEL protein).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                      conditions (By similarity).
-!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of a subunits (By similarity).
-! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-! SIMILARITY: Belongs to the chaperonin (HSP60) family.
                                                                                                                    Bacteriā; Proteobacteria; Gammaproteobacteria; Legionellales;
Legionellaceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           551 AA; 58332 MW; A25895CBF9585DA0 CRC64;
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PIR; JC2562; JC2562.
HASSP; P06139; IGRL.
HAMAP; MC 00600; -; 1.
InterPro; IPR001844; Chaprnin Cpn60.
InterPro; IPR002423; Cpn60/TCF-1.
Pfam; PF00118; Cpn60 TCF1; 1.
PRINTS; PR00298; CHAPERONING.
PRINTS; PR00304; TCOMPLEXTCP1.
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                                                                                                     SEQUENCE FROM N.A.
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Chaperone; ATP-binding; Heat B
SEDUENCE 547 AA; 57610 MW;
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PRINTS; PR00304; TCOMPLEXTCPI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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522 Aspieu-----ProlyslysaspGluGlyMetalaGlyAalaGlyAspMetGlyGlyMet
                                                                          1507 GCATTACAAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGCGCTATTGCT
                                                                                                             (Heat shock protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 51684;
MEDLINE=97419519; PubMed=9274034;
Haake D.A., Summers T.A., McCoy A.M., Schwartzman W.;
"Heat shock response and groEL sequence of Bartonella henselae and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings 7 subunits (By similarity).
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Bartonellaceae; Bartonella.
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30-MAY_2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
60 kDa chaperonin (Protein Cpn60) (groEL protein)
                                                                                                                                                                                  1567 GAAAAACCAGAACCTAAAAAAGATATGCCTATGCCTGGG
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HSSP; P06199; 1GRL.
HAMAP; MF 00600; -; 1.
InterPro; IPR001844; Chaprnin Cpn60.
InterPro; IPR002423; Cpn60/TCP-1.
Pfam; PF00118; Cpn60_TCP1: 1.
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AATAICAICCGICGITCTTTGAAGAGCCTITTACGICAAATIGCTGCAAAIGCTGGCTAI 1380
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                                                                                                        AATGCAACAAGAGCTGCGGTTGAAGAAGGTATTGTCCCTGGTGGTGGTACTGCTTTTGTC 1260
                                                                                                                                                          CGCTCCATTAAAGTCCTTGATGATATTAAACCTGCTGATGATGATGAACTTGCTGGACTT 1320
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  GATCGTGAAAAACTTCAAGAACGTCTTGCAAAAACTTGTTGGTGGAGTAGCTGTTATCCAT
                    GTTGGAGCTGCTACTGAAACTGAAATGAAAGAGAAGAAGAATCGTGTAGAAGATGCTCTA
                                                                             381 ValGlyGlyAlaThrGluValGluValLySGluLySLySAspArgValAspAspAlaLeu
                                                                                                                       Bacteria; Proteobacteria, Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
60 No chaperonin 4 (Protein Cpn60 4) (groEL EGROL4 OR GROEL4 OR RA0395 OR SMA0744.
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MEDLINE=21396509; PubMed=11481432;
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                                        Aspile_ieuAlaAsnAlaValLysValThrLeuGlyProLysGlyArgAsnValValIle
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HAMAP; MF 00600; -; 1.

InterPro; IPR001844; Chaprnin Cpn60.

InterPro; IPR002423; Cpn60/TCP-1.

Pfam; PF00118; cpn60 TCP1; 1.

PRINTS; PR00298; CHAPERONING.

PRINTS; PR00304; TCOMPLEXTCP1.

PROSITE; PS00296; CHAPERONINS_CPN60; 1.

Chaperone; AFF-binding; Heat shock; Multigene family; Plasmid; SEQUENCE 545 AA; 57701 MW; 49BA61F23CE70431 CRC64;
 SIMILARITY: Belongs to the chaperonin (HSP60) family.
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Best Local Similarity:
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              TTTGGTGAACGCCGTAAAGCTATGCTTGAAGATATTGCTATCCTTACTGGAGGAGAAGCA
                                               CTTTGTAATGAGAAAAAATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTT
                                                                                               GCTAAAAGTAAAACCGTCCACTCCTTATTATTGCTGAAGACGTAAAAGGTGAAGCACTTGCA
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                                                                                                                                    conditions (By similarity).
-!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of 7 subunits (By similarity).
-!- SUBCELLULAR LOCATION: Qytoplasmic (By similarity).
-!- SUBCELLULAR LOCATION: to the chaperonin (HSP60) family.
                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress
                                                                         Xylella fastidiosa.Bacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSEP, PO6139; IGRL.
HAMAP; MF_00600; -; 1.
InterPro; IPR001844; Chaptnin Cpn60.
InterPro; IPR001842; Cpn60/ICP-1.
Pfam; PF00118; cpn60 TCP1; 1.
PRINTS; PR00298; CHAPERONIN60.
PRINTS; PR00394; TCOMPLEXTCP1.
PROSITE; PS00396; TCOMPLEXTCP1.
Chaperone; ATP-binding; Complete proteome.
SEQUENCE 547 AA; 57757 MW; 30BE7F937CA7A9D8 CRC64;
                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
60 kDa chaperonin (Protein Cpn60) (groEL protein)
        A
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                                                                                            Xanthomonadaceae; Xylella
                                                                GROL OR GROEL OR XF0615.
        STANDARD;
                                                                                                                        SEQUENCE FROM N.A.
                                                                                                      NCBI_TaxID=2371;
                                                                                                                                  STRAIN=9a5c
       CH60 XYLFA
CH60 XYLFA
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347
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80
97
2
               Matches:
Conservative:
                                                       Mismatches:
                                                                             Indels:
                                                                                                                                  US-09-077-574A-1 (1-1647) x CH60_XYLFA (1-547)
   9.22e-96
             1862.50
81.39%
66.79%
62.75%
                                     Percent Similarity:
Best Local Similarity:
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                                                                                                  GATCGTGAAAAACTTCAAGAACGTCTTGCAAAACTTGTTGGTGGAGTAGCTGTTATCCAT 1140
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      AAACGIGIAGITATIGACAAAGAAAATACTACTATGGITGAIGGIGCIGGAAAAICAGAA 1020
                                                    GATATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTAT 1080
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                                                                 AspArgGluLysLeuGlnGluArgValAlaLysLeuAlaGlyGlyValAlaValIleLys 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thoroifsdottir E.T.T., Backman V.M., Blondal T.,
Thorbjarnardottir S.H., Palsdottir A., Hauksdottir H.,
Kristjansdottir S., Eggertsson G.;
"Heat shock in Rhodothermus marinus: cloning and sequence analysis
"Heat shock in Rhodothermus marinus: cloning and sequence analysis
submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Prevents misfolding and promotes the refolding and
proper assembly of unfolded polypeptides generated under stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhodothermus marinus (Rhodothermus obamensis).
Bacteria, Bacteroidetes, Sphingobacteria, Sphingobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
60 kDa chaperonin (Protein Cpn60) (groEL protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             540 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Bacteroidetes; Sphin
Crenotrichaceae; Rhodothermus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 ThrAlaGlyLeuLysServalThrAlaGlyAlaAsnProMetAspLeuLysArgGlyIle 120
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141 LysAsnarg1leAlaGlnValAlaThrIleSerAlaAsnGlyAspLysAlaIleGlyGln 160
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                       SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of 7 subunits (By similarity).
SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 AsplysbeualaaspalaValLysValThrLeuGlyProLysGlyAxgAsnValIleIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        686744BB7BEF18EC CRC64;
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE, PS00296, CHAPERONINS_CPN60; 1.
Chaperone; ATP-binding.
SEQUENCE 540 AA; 57666 MW; 6867448B
                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP; MF 00600; -; 1.
InterPro; IPR001844; Chaprnin Cpn60.
InterPro; IPR00243; Cpn60/TCP-1.
Pfam: PF00118; cpn60 TCP1; 1.
PRINTS; PR00298; CHAPERONIN60.
PRINTS; PR00304; TCOMPLEXTCP1.
                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF145252; AAD37976.1; -.
conditions (By similarity)
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82.46$
69.22$
62.42$
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546 AA

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STANDARD;
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LysGlyThrGluThrThrLeuGluValValGluGlyMetGlnPheAspArgGlyTyrLeu
                                    TCTCCATACTTTGTAACTAATCCTGAGAAAATGGTTTGTGAAACTTGATAACCCTTATATC
                                                                                CTTTGTAATGAGAAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTT
                                                                                                                           721 GCTAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCA
                                                                                                                                                                      ACACTTGTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGT
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RESULT 15 CH60_CHRVI

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=93186721; PubMed=8444812;
Ferreyra R., Soncini F., Viale A.M.;
Forning, characterization, and functional expression in Escherichia coli of chaperonin (groESL) genes from the phototrophic sulfur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dionisi H.M., Viale A.M.; "Purification and characterization of Chromatium vinosum GroEL and GroES proteins overexpressed in Escherichia coli cells lacking the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endogenous großEL operon.",
Protein Expr. Purif. 14:275-282(1998).
-!- FUNCTION: Prevents misfolding and promotes the refolding proper assembly of unfolded polypeptides generated under conditions.
                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP, ME 00600; -; 1.

InterPro; IPR001844; Chaprnin Cpn60.

InterPro; PR00243; Cpn60/TCP-1.

Fram; PF00118; cpn60 TCP1; 1.

PRINTS; PR00298; CHAPERONIN60.

PRINTS; PR00295; CHAPERONINS_CPN60; 1.

Chaperone; ATP-binding.

SEQUENCE 546 AA; 57541 MW; 3250141881C04DD6 CRC64;
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374
70
101
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
28-FBB-2003 (Rel. 41, Last amotation update)
60 kDa chaperonin (Protein Cpn60) (groEL protein)
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         bacterium Chromatium vinosum.";
J. Bacteriol. 175:1514-1523(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99008942; PubMed=9790891;
                                                                                                                                                                                                          Chromatiaceae; Allochromatium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M99443; AAA23319.1; -.
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HSSP; P06139; 1GRL.
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ò	1201 AATGCAACAAGAGCTGCGGTTGAAGGTATTGTCCCTGGTGGTGGTGTTGTCTTTTTTC 1260
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ολ	1261 CGCTCCATTAAAGTCCTTGATGATATTAAACCTGCTGATGATGAAGAACTTGCTGGACTT 1320
QQ	::: 421 ArgAlaIleAlaAlaYalLySASpLeuLysGlyAlaAsnHisAspGlnAspValGlyIle 440
λõ	1321 AATATCATCCGTCGTTCTCTTGAAGAGCCTTTACGTCAAATTGCTGCAAATGCTGGCTAT 1380
qq	441 AlaileAlaArgArgAlaMetGluGluProLeuArgGlnIleValAlaAsnAlaGlyGlu 460
δλ	GAAAAAGTTCGTGAACCAAAAGATGGTTTTGG
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δλ	GAGAATATGAAGACCTTATTAAAGCTGG
Dþ	481 AlaAsnGlyGluTyrGlyAspMetValGluMetGlyIleLeuAspProThrLysValThr 500
Qy	GCATCAGTAGCCTCCTTA
qq	501 ArgSerAlaLeuGlnAsnSerCysSerValAlaGlyLeuMetlleThrThrGluAlaMet 520
λδ	1561 ATTGCTGAAAAACCAGAACCTAAAAAAGATATGCCTATGCCTGGGGGTGGTATGGT 1617
qq	521 IleAlaAspGluProLysAspAspAlaProAlaMetProGlyGlyGlyMetGly 538
Οy	1618 GGTATGGGTGTATGGACGGTATG 1641
qq	539 AspMetGlyGlyMetGlyMetMet 546
Search Tob time	Search completed: January 28, 2004, 13:26:11

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Q8Kiy3 streptococc
Q8Kij2 streptococc
Q9Kar5 streptococc
Q9Gpc2 enterococcu
Q8Kj08 streptococcu
Q8721 bartonella
Q8gpc8 enterococcu
Q8gbb enterococcu
Q8gb0 streptococcu
Q8gy00 tusobacteri
Q8cwj0 vibrio vuln
Q8gbd2 acetobacter
Q8kj46 rhizobium 1
Q8ks77 brucella su
Q8gb95 heliobacill
Q9ajb5 pseudoalter
                                                                                                                                                   Q93fu8 enterobacte
O33688 primary end
Q8rnu2 helicobacte
Q8kiw5 buchnera sp
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Q8kiw2 buchnera sp
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29rc20 bacillus sp
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helicobacte
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09ezv4 bacillus st
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-!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDMed=9720028; MEDMED: WEDLINE=9838497; PubMed=9720028; Morrow C.J., Reed M.B., Hasse D., Strugnell R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
GroEL/HSP60 homolog (60 kDa chaperonin) (Protein Cpn60) (groEL
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Q8GBB4
 Q8GBD2
Q8KJ46
Q8FX87
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Q8CWW6
Q8KIW2
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Q8CXL3
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Q8GBD0
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Q8GBC6
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Q9X4R5
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Q9AJB5
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Q8KIW5
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Q8KIW3
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Q8KJ08
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Q8KIW7
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Q8GBC8
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                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08,
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                                            Plasmid pISI-2
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ODDELEFrame+ n2P model - DEV=xlp
-0=\text{ODDELEFrame+ n2P} model - DEV=xlp
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                            protein search, using frame plus n2p model
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SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS 7 SUBUNITS (BY SIMILARITY). SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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INCEPPC; IPRO01444; Chaprnin Cpn6.
INCERPC; IPR002423; Cpn60/TCF-1.
Pfan; PF00118; cpn6 TCP1; 1.
PRINTS; PR00299; CTAPERCNING.
PRINTS; PR00304; TCOMPLEXTCP1.
PROSITE; PS00296; CTAPERCNINS CPN60; 1
ATP-binding; Chaperone; Plasmid.
SEQUENCE 548 AA; 58605 MW; 6388C43
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                                                         Okamoto-Kainnma A., Yan W., Kadono S., Tayama K., Koizumi Y., Yanagida F., Yanattaration of groEL Operon in Acetobacter aceti."; J. Biosci. Bioeng. 94:140-147(2002).
EMBL, AB081586; BAC16232.1; -. SEQUENCE 546 AA; 58106 MW; 3E476AF42F2CD5CC CRC64;
                                                                                                                                                                                                                                         1 ATGCCTTCTAAAGAAATCCTTTTTGATGCTAAAGCCCGTGAAAAACTTTCACGAGGTGTA
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Conservative:
Mismatches:
Indels:
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         Acetobacteraceae; Acetobacter
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1880.00
82.42%
69.78%
63.34%
                                       SEQUENCE FROM N.A.
                                                                                                                                                                             Similarity:
                  NCBI_TaxID=435;
                                                   STRAIN=IFO3283;
                                                                                                                                                                  Percent Similarity:
                                                                                                                                   Alignment Scores:
Pred. No.:
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                                                                      ACACTTGTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGT
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Probable chaperonin groEL DF protein (60 kDa chaperonin) (Protein
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                                                                                                                               Mesorphizobium loti strain R7A.";

J. Bacteriol. 184:3086-3095(2002).

J. Bacteriol. 184:3086-3095(2002).

PROPER ASSEMBLY OF UNFOLDED FOLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).

C. -I SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF THE SUBUNIT: OLIGOMER OF THE CHAPERONIN (HSP60) FAMILY.

REMBL, ALGORISTY: BELCONGS TO THE CHAPERONIN (HSP60) FAMILY.

REMBL, ALGORISTS: CAD312311;

REMBL, ALGORISS: CAD60/TCF-1.

REMBL, PRO0118; PRO02423; CDn60/TCF-1.

REMBLS: PRO0298; CHAPERONING.

PRINTS; PRO0294; TCOMPLEXTCF1.
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                                                                      MEDLINE=21999272; PubMed=12003951;
Sullivan J.T., Trzebiatowski J.R., Cruickshank R.W., Gouzy J.,
Brown S.D., Elliot R.M., Fleetwood D.J., McCallum N.G., Rossbach U.,
Stuart G.S., Weaver J.E., Webby R.J., de Bruijn F.J., Ronson C.W.;
"Comparative sequence analysis of the symbiosis island of
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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                                                               GATATTAAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTAT
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                                           <u>AAAGGTCTTGAAACTACATTAGATGTGGTTGAAGGAATGAAGTTTGACCGTGGCTACCTC</u>
                                                                                                                          TCTCCATACTTTGTAACTAATCCTGAGAAATGGTTTGTGAACTTGATAACCCTTATATC
                                                                                                                                                                                                                                                                                            GCTAAAGTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCA
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SEQUENCE FROM N.A.

STRAIN-1330 / Biovar 1;

MEDLINE-22247741; PubMed=12271122;

Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,

Paulsen I.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,

Daugherry S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,

Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J. van Aken S.E.

Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,

HOOVER D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;

"The Brucella suis genome reveals findamental similarities between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATAAACTTGCAAATGCTGTTAAAGTAACACTTGGACCTAAAAGGCCGTAATGTCGTTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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377
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Last annotation update)
1600 CCTGGCGCTGGTATGGGTGGTATGGGTATGGAC 1635
                                                                                                                                                                                                                                                                                                        animal and plant pathogens and symbionts.";
Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002)
EMBL; AE014521; AAN33401.1; -.
           540 GlyGlyGlyGlyMetGlyGlyMetGlyGlyMetAsp 551
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Matches:
Conservative:
Mismatches:
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                                                                                      Created)
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                                                                     08FX87;
01-MAR-2003 (TrEMBLrel. 23, C
01-MAR-2003 (TrEMBLrel. 23, i)
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1819.00
80.33%
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61.29%
                                                              PRELIMINARY;
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NCBI_TaxID=29461;
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                                                                                                                             GROEL OR BRA0195.
Brucella suis.
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                                                                                             ATCATAGCTGAAGCTATGGCTAAAGTTGGAAAAGGAGGTGTTATCACAGTTGAGGAAGCT
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| AlaLysMetThrValPheAsnGluGluAlaArgArgAlaLeuGluLysGlyValAsnThr
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                                                                                    519 AlametileAlaGluLeu-----ProLysLysAspAlaAlaProAlaGlyMetProGly
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Licourne From N.A.
Licourne K.G., Chu L., Ostrovskaya O., Mendybaeva N., Koukharenko V., Gerdes S., Kyrpides N., Overbeek R.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY142910; AAN87514.1;
NON TER 545 545
                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
60 kDa chaperonin groEL (Fragment).
Heliobacillus mobilis.
Bacteria; Firmicutes; Clostridia; Clostridiales; Heliobacteriaceae;
Heliobacillus.
NCBL_TAXID=28064;
                                                         TGCGCTATTGCTGAAAAACCAGAACCTAAAAAAAAAAATATGCCTATGCCTGGC
                                                                                                                                                                                                                                                                                                                                                                               Raymond J., Zhaxybayeva O., Gogarten J.P., Gerdes S.Y., Blankenship N.E.; "Whole-genome analysis of photosynthetic prokaryotes."; Science 298:1616-1620(2002).
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1804.50
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                                                                         GAAATAGCTCAAGTTGGAACCATTTCTGCAAACTCTGATACAACAATAGGTAATATCATA
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1447 GGAGAATATGAAGACCTTATTAAAGCTGGTGTCATTGATCCTAAAAAAGTTACACGTATT 1506
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Kurusu Y., Nakamura T.;

Kurusu Y., Nakamura T.;

Kurusu Y., Nakamura T.;

Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNPOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).

-! SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).

-! SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.

EMBL; AB057417; BRB39465.1;

HSSP; P06139; 1GRL.
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                                            GCATTACAAAAIGCAGCAICAGTAGCCICCTTACTTCTAACTACAGAAIGCGCTATIGCT
                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Alteromonadaceae, Pseudoalteromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
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360
79
108
                                                                                                                                                                                                                       Q9AJB5;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
groEL protein (60 kDa chaperonin) (Protein Cpn60).
GROEL.
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Matches:
Conservative:
Mismatches:
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InterPro; IPR002423; Cpn60/TCP-1.
Pfam; PF00118; opn60_TCP1; 1.
PRINTS; PR00298; CHAPERCONINGO.
PRINTS; PR00304; TCOMPLEXTCP1.
                                                                                                                                         GGTATGGAC --- GGTATG 1641
                                                                                                                                                               540 GlyMetAspMetGlyMet 545
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1796.50
80.11%
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SEQUENCE FROM N.A.
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181 GAACTIGAAGAIAAGITITGAAAAIATGGGCGCTCAAAIGGITAAAGAAGIAGCTCCCAAA
                       421 CAAAAAGAAATAGCTCAAGTTGGAACCATTTCTGCAAACTCCTGATACAACAATAGGTAAT
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GICCGCICCATIAAAGICCIIGAIGAIAIIAIAAACCIGCIGAIGAIGAIGAACIIGCIGGA
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|ValArgAlaAlaSerLysLeuValGluLeuClyAspAspAsnGluAspGlnAsnHisGly
                                           CTTAATATCATCCGTCGTTCTCTTGAAGAGCCTTTACGTCAAATGCTGCAAATGCTGGC
                                                        STRAIN=WR-1;

MEDLINE=22297686; PubMed=12368813;

Meidlberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,

Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,

Meyer T., Taspin A., Scott J., Beanan M., Brinkac L., Daugherty S.,

Deboy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,

Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,

Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,

Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,

Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.,

"Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                         1558 GCTATTGCTGAAAAACCAGAACCTAAAAAAGATATGCCTATGCCTGGCGGTGGTATGGGT
                                                                                                                                                Shewanella oneidensis.
Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
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Last annotation update)
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                              Created)
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59.99%
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                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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SEOUENCE 545 AA:
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Best Local Similarity:
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GlnAlaLeuGluAsnGluLeuAspValValGluGlyMetGlnPheAspArgGlyTyrLeu
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                                                                                                                                                                                                                                                                             441 ValileAlaLeuArgAlaMetGluAlaProLeuArgGlnIleAlaThrAsnAlaGlyGlu 460
                         381 ValGlyAlaAlaThrGluValGluWetLysGluLysLysAlaArgValGluAspAlaLeu
GTTGGAGCTGCTACTGAAACTGAAATGAAAGAGAAGGAATCGTGTAGAAGATGCTCTA
                                                                             AATGCAACAAGAGCTGCGGTTGAAGAAGGTATTGTCCCTGGTGGTGGTACTGCTTTTTGTC
                                                                                                                                                          CGCTCCATTAAAGTCCTTGATATTAAACCTGCTGATGATGATGATGACTTGCTGGACTT
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STRAINLY,
STRAINLY,
FERAT J.-L., Legouar M., Michel F.;
Ferat J.-L., Legouar M., Michel F.;
Ferat J.-L., Legouar M., Michel F.;
For Strop II intron has invaded the genus Azotobacter inserted within the sesential grobL gene.";
Submitted (NOY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY057439; AAL25964.1;
SEQUENCE 546 AA; 56875 MW; BEIF4CC93E42A619 CRC64;
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Last annotation update)
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Mismatches:
Indels:
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"Group II self-splicing introns in bacteria.";
Nature 364:358-361(1993).
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MEDLINE=93323980; PubMed=7687328;
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1780.50
79.63%
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SEQUENCE FROM N.A.
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Best Local Similarity:
Query Match:
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Pred. No.:
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PRINTS; PR00304; TCOMPLEXTCP1
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             PROSITE; PS0(
ATP-binding;
                                                          Alignment Scores:
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STRAIN-MS;

Kondo A., Yohda M.;

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).

-!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.

HSSP; P06139; 1GRL.
                                                                                                                                                                                                                                                                                                                                                                 CGTATTGCATTACAAAATGCAGCATCAGTAGCCTCCTTACTTCTAACTACAGAATGCGCT
                                                     501 ArgSerAlaLeuGlnAlaAlaSerSerIleGlyGlyLeuMetIleThrThrGluAlaMet
                                                                                                                               AATGCAACAAGAGCTGCGGTTGAAGAAGGTATTGTCCCTGGTGGTGGTACTGCTTTTGTC
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                                                                                  GITGGAGCTGCTACTGAAACTGAAATGAAAGAAGAAGGATCGTGTAGAAGATGCTCTA
                                                                                                       381 ValGlyAlaAlaThrGluValGluMetLysGluLysLysAlaArgValGluAlaAlaLeu
                                                                                                                                           Bacillales; Bacillaceae; Bacillus
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last amotation update)
Protein Cpn60 (60 kDa chaperonin) (groEL protein).
CPN60.
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InterPro; IPR002423; Cpn60/TCP-1.
Pfam: PF00118; Cpn60 TCP1; IPPRINTS; PR00298; CHAPERONINGO.
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Bacteria; Firmicutes;
NCBI_TaxID=96470;
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                                                                                                                                                                                                                                                                    7 TCTAAAGAAATCCTTTTTGATGCTAAAGCCCGTGAAAAACTTTCACGAGGTGTAAAA
                                 539 AA; 57346 MW; 95626C980E30C46F CRC64;
                                                                                           Conservative:
Mismatches:
Indels:
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Matches:
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PS00296; CHAPERONINS_CPN60; 1.
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                                                                                         6.62e-85
1768.00
80.55$
64.95$
                 Chaperone.
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Best Local Similarity:
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                                                                                                                    AAAGCTCGAGTTAAACAAATTCGTGCACAAATTGAAGAAACAAGCTCAGATTATGATCGT 1086
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                                            GluGluLeuGlyArgGluLeuLysSerAlaThrIleAlaSerLeuGlyArgAlaSerLys 320
AspargarglysAlaMetLeuGluAspIleAlaIleLeuThrGlyGlyGluValIleSer 300
                                                                                    GluLysLeuGlnGluArgLeuAlaLysLeuAlaGlyGlyValArgVallleLysValGly
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|SerValIleValGluArgLeuLysThrGluLysProGlyIleGlyPheAsnAlaAlaThr
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                       GAAGATCGTGGTATAAAGCTTGAAAATGTAAGCTTGTCTTTTAGGAACAGCTAAACGT
                                                                       GTAGTTATTGACAAAGAAAATACTACTATCGTTGATGGTGCTGGAAAATCAGAAGATATT
                                                                                                                                                                                                                                                                                      401 ThrargalaalavalGluGluGlyilevalalaGlyGlyThralaLeuMetAsnVal
                                                                                                                                                                                                                                                                                                              Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira
NCBL_TaxID=173;
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Heat shock protein 58 (60 kDa chaperonin) (Protein Cpn60)
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PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).

-!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.

EMBL, AF032910, AAB86965.1; -.

HSSP; P06139; 1GRL.
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                                                                                                                                                                                                                                                                                                                       546 AA; 57969 MW; 15BC9EC0A8E2A6E3 CRC64;
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Matches:
Conservative:
Mismatches:
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InterPro; IPR002423; Cpn60/TCP-1.
Pfam; PR00118; Cpn6 TCP1; 1.
PRINTS; PR00298; CHAPERSONIN60.
PRINTS; PR00304; TCOMPLEXTCP1.
PROSITE; PS00296; CHAPERONINS_CPN60; 1.
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1768.00
80.07%
64.35%
59.57%
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             GluLysLeuGlnGluArgLeuAlaLysLeuAlaGlyGlyValAlaVal11eHisValGly
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                                                  GTAGTCAATAAGCTCCGTGGAGCACTCCAAGTTGTAGCCGTAAAAGCTCCTGGTTTTGGT
                                                                                                                                                    GAAGAICGIGGIATAAAGCITGAAAAIGTAAGCITGICTTCTTTAGGAACAGCTAAAACT
                                                                                                                                                                           GluAspLeuGlyMetLysLeuGluAsnThrThrLeuGlnMetLeuGlyArgAlaAsnLys
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O9EZV4; 01-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) groEL protein (60 kDa chaperonin) (Protein Cpn60).

539 AA

PRELIMINARY;

Q9EZV4

E PT PT PE

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| 122 AlaValAlaValAlaValGluGluLeuLysAlaIleSerLysProIleGlnGlyLysGlu 141
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                                                                                                                                                   22 LeuAlaAspAlaValLysValThrLeuGlyProLysGlyArgAsnValValLeuGluLys
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                                                                                                                   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER
                                                                                                                                                                                                                                                                                                             539 AA; 57293 MW; 2F51B6FFBB887428 CRC64;
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                                                                                 Snapyan M., Gochikyan A., Weigel P., Sakanyan V.; "Effect of thermostable chaperonins on synthesis o
                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
                       Bacteria; Firmicutes; Bacillales; Geobacillus.
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Matches:
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1754.00
80.55%
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59.10%
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Query Match:
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                              181 PheThrThrGluLeuAspValValGluGlyMetGlnPheAspArgGlyTyrAlaSerPro
                                                                                                                            667 AATGAGAAAAGATTACTAGCATGAAAGACATGCTACCAATCTTAGAACAAGTTGCTAAA
                                                                                                                                                                                                                            GAACGCCGTAAAGCTATGCTTGAAGATATTGCTATCCTTACTGGAGGAGAAGCAATATTT
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  CTTGAAACTACATTAGATGTGGTTGAAGGAATGAAGTTTGACCGTGGCTACCTCTCTCCA
                                                                                                TACTTTGTAACTAATCCTGAGAAAATGGTTTGTGAACTTGATAACCCTTATATCCTTTGT
                                                                                                                                                                                                                                                                                              GTAAACCGTCCACTCCTTATTATTGCTGAAGACGTAGAAGGTGAAGCACTTGCAACATT
                                                                                                                                                                                                                                                                                                                            241 GlnGlyLysProLeuLeuLeullelleAlaGluAspValGluGlyGlyBlaLaLeuAlaThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                  261 ValValAsnLysLeuArgGlyThrPheThrAlaValAlaValLysAlaProGlyPheGly
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RAY YOSHIGA N., Ocda K., Watanabe E., Mikami T., Fukita Y., Nishimura K., RA Komai K., Matsuda K.; Komai K., Matsuda K.; Romai K., Matsuda K.; Ratsuda K.; Matsuda K.; Matsuda K.; Romai K., Matsuda K.; Romai K., Matsuda K.; Ratsuda K.; Matsuda K.;
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41 AspLysSerPheGlyAlaProThr1leThrLysAspGlyValSerValAlaArgGluIle
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                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacter aerogenes (Aerobacter aerogenes).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Enterobacter.
                                                                                                                                                                                                                                                                                                                (groEL
                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MRA-2003 (TrEMBLrel. 23, Last amnotation update)
groEL-like protein (60 kDa chaperonin) (Protein Cpn60)
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Mismatches:
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ATP-binding; Chaperone.
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1627 GGTATGGACGGTATG 1641
                                               534 AspMetGlyGlyMet 538
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1742.00
78.02%
64.65%
58.69%
                                                                                                                                                                       PRELIMINARY;
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Best Local Similari
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Biochem. Biophys. Res. Commun. 239:769-774(1997).
-!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARIY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae.
NCBI_TaxID=2342;
                                                                                                                                                                                                                                                                                                                                                                                                 groEL protein (60 kDa chaperonin) (Protein Cpn60) (Fragment). GROEL.
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-1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
EMBL, AF005236, AAB97670.1; -.
HSSP, F06139, LOON.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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InterPro; IPR002423; Cpn60/TCP-1.
Pfam; PR00118; cpn60 TCP1; 1.
PRINTS; PR00298; CHAPERONIN60.
PRINTS; PR00304; TCOMPLEXTCP1.
PROSITE; PS00296; CHAPERONINS_CPN60; 1.
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                                                  401 HisAlaThrArgAlaAlaValGluGluGlyValValAlaGlyGlyGlyValAlaLeuIle
                                                                                                                                                                             481 AlaThrGluGluTyrGlyAsnMetIleAspMetGlyIleLeuAspProThrLysValThr
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                                                                                                                                      CGCTCCATTAAAGTCCTTGATGATATTAAACCTGCTGATGATGATGAACTTGCTGGACTT
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: PREVENTS MISSOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRE CONDITIONS (BY SIMILARITY).
7 SUBUNIT: OLIGOMER OF SUMILARITY).
8 SUBUNITS (BY SIMILARITY).
8 SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=20123532; PubMed=10660136;
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1387 TCTATTGTTGTAGAAAAGTTCGTGAACCAAAAGATGGTTTTGGATTTAATGCTGCATCA 1446
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                                                382 AlaAlaSerGluValGluMetLysGluLysLysAspArgValAspAspAlaLeuSerAla
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                                                                                                          GAAGATCGTGGTATAAAGCTTGAAAATGTAAGCTTGTCTTCTTTAGGAACAGCTAAACGT
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73
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Matches:
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EMBL, AF479030; AAL86900.1; -.
InterPro; IPR001844; Chaprnin Cpn60.
InterPro; IPR002423; Cpn60/TCP-1.
PFam; PF00118; cpn60 TCP1; 1.
PROSITE; PS00296; CHAPERONINS_CPN60; ATP-binding; Chaperone.
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                                                                                                       PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY)

-!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF TRUBY SIMILARITY)

-!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.

EMBL; AJ344978; CAC86959.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                          GluLeuGluAspLysPheGluAsnMetGlyAlaGlnMetValLysGluValAlaSerLys
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                                                                                                                                                                                                                                                                                                                                                                                                41 AsplysSerPheGlyAlaProSerlleThrLysAspGlyValSerValAlaArgGlulle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Delmotte F., Sabater B., Simon J.C., Latorre A.; "Coevolution between mitochondrialand simbiotic DNA at intraspecific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaAsnAspAlaAlaGlyAspGlyThrThrAlaThrLeuLeuAlaGlnSerIleVal
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Thesis (2001), University of Valencia, Spain.
-!- FUNCTION: PREVENTS MISPOLDING AND PROMOTES THE REFOLDING AND
                              Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                      659886423C19529D CRC64;
                                                                                                                                                                                                                                                                                       548
338
92
114
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Matches:
Conservative:
Mismatches:
Indels:
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ATP-binding; Chaperone.
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                                                                                                                                                                  EMBL, AJ344918, CAC86559.1; -.
LILEETPRO, IPRO01844; Chaptnin Cph60.
InterPro, IPR002423; Cpn60/YCF-1.
Pfam; PF00118; cpn60 TCP1; 1.
PRINTS; PR00298; CHAPERONINGO.
PRINTS; PR00304; TCOMPLEXTCP1.
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1714.50
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241 AlalysSerGlyLysProLeuLeullelleSerGluAspLeuGluGlyGluAlaLeuAla
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Search completed: January 28, 2004, 13:28:47 Job time : 98 secs

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January 28, 2004, 13:10:00 ; Search time 47 Seconds (without alignments) 1850.684 Million cell updates/sec
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IES	Description	Lawsonia intracell		1	I	I		7	I	
SUMMARIES	ID	AAW16678	AAY23930	AAY23909	AAB69060	AAR67381	AAB69061	AAY23915	AAY75747	ABP77245
		18	20	20	22	16	22	20	21	24
	Query Match Length DB	548	545	549	547	547	574	545	544	544
ď	Query Match	100.0	68.9	68.2	67.4	67.2	67.2	67.0	6.99	66.7
	Score	2708	1864.5	1848	1825.5	1820.5	1819	1814.5	1812.5	1805.5
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H		64.5	545	21	AAB19080	Amino acid sequenc	equenc
17		4.	548	19	AAW65070	E. coli Groel	L prot
ĭ		64.5	548	20	AAW95001	WO9902989 Seq	
16		4	548	22	AAB50536	Escherichia	coli G
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<u> </u>		64.4	545	23	ABB99013	_	organi
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5.		64.3	545	23	ABB99012	al	organi
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2		64.3	548	19	AAW61378	GroEL N-terminal	inal r
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7	Н	64.1	548	20	AAY23908	Amino acid sequenc	equenc
28		64.1	548	16	AAR67382	E. coli GroEL gene	L gene
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3(64.0	545	20	AAY23901	Streptococcus pneu	naud s
3,		64.0	542	23	ABB49241	Listeria monocytog	ocytog
3,	Н	63.9	544	20	AAY23903	Streptococcus pyog	Boyd 8
33	Н		546	14	AAR41661	H. pylori hs	p60.
34	Н	63.6	546	14	AAR41200	Hsp. Helicobacter	bacter
36			544	12	AAR13337	HypB protein.	. chl
36	Н		546	19	AAW98776		PO 118
3,			548	23	ABB99019	Detrimental o	organi
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44	71	63.1	544	22	AAE11757	Chlamydophila	a pneu
4	5 1710	63.1	544	23	ABB94272	Chlamydia pne	

ALIGNMENTS

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Intestinal disease; porcine proliferative enteropathy; vaccine; GroEL; immunotherapy; antibody; diagnosis; heat shock protein.
                 AAW16678 standard; Protein; 548 AA
                                                                         Lawsonia intracellularis GroEL.
                                                                                                                                                                              96WO-AU00767.
                                                                                                                                                                                                95AU-0006911.
95AU-0006910.
                                                                                                                                                                                                                           (DARA-) DARATECH PTY LTD. (PIGR-) PIG RES & DEV CORP.
                                                      (first entry)
                                                                                                                      Lawsonia intracellularis.
                                                                                                                                                                                                                                                        Hasse D, Panaccio M;
                                                                                                                                                                                                                                                                          WPI; 1997-310605/28.
N-PSDB; AAT69201.
                                                                                                                                          WO9720050-A1.
                                                                                                                                                                             29-NOV-1996;
                                                                                                                                                                                                30-NOV-1995;
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                                                      20-AUG-1997
                                                                                                                                                            05-JUN-1997
                                   AAW16678;
RESULT 1
         AAW16678
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Heat shock protein; Hsp; immune response; immunological carrier;

Consensus mino acid sequence of a heat shock protein.

cancer control; tumour; sarcoma; cancer; gene therapy

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can be used in vaccines to protect birds and animals against intestinal diseases, esp. to protect pigs against porcine proliferative enteropathy. It is the expression product of a DNA molecule (AAT69201) obtd. by screening an L. intracellularis library with rabbit anti-L. intracellularis sera. GroEL, GroES (AAW16679) and other L. intracellularis polypeptides (AAW16680-85) can be administered as recombinant polypeptides or expressed as Accombinant vaccines utilising bacterial, fungal or viral vectors. Antibodies raised against the polypeptides may be useful in immunotherapy, diagnosis of infection and detection.
                                                                                                                                             The GroEL heat shock protein (AAW16678) of Lawsonia intracellularis
                        ð
Vaccine for treating or preventing Lawsonia intracellularis infection - especially in pigs, containing non-pathogenic form bacterium or its components
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 18; Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 2708; DB 18;
100.0%; Pred. No. 3.4e-170;
live 0; Mismatches 0;
                                                                                                  Claim 10; Page 38-42; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    548 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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useful in vaccines, as carriers for other immunogens, as anticancer agents and for diagnosis New nucleic acid encoding heat shock protein-60 from Streptococcus,

Disclosure, Fig 10A-E; 176pp; English.

(STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

Wisniewski J;

Mizzen L,

WPI; 1999-430397/36.

Local Similarity

98WO-CA01203 97US-0001737

29-DEC-1998; 31-DEC-1997;

WO9935270-A1

Synthetic.

15-JUL-1999,

ö DREKLOERLAKLVGGVAVIHVGAATETEMKEKKDRVEDALNATRAAVEEGIVPGGGTAFV 420 DKAVVAVTKELSDITKPTRDQKEIAQVGTISANSDTTIGNIIAEAMAKVGKGGVITVEEA 180 181 KGLETTILDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQV 240 AKVNRPLLIIAEDVEGEALATLVVNKLRGALQVVAVKAPGFGERRKAMLEDIAILTGGEA 300 301 IFEDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDY 360 9 09 ASGEYEDLIKAGVIDPKKVTRIALQNAASVASLLLTTECAIAEKPEPKKDMPMPGGGMGG ASGEYEDLIKAGVIDPKKVTRIALQNAASVASILLITTECAIAEKPEPKKDMPMPGGGMGG RSIKVLDDIKPADDDELAGLNIIRKSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNA DKAVVAVTKELSDITKPTRDQKEIAQVGTISANSDTTIGNIIAEAMAKVGKGGVITVEEA KGLETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQV AKVNRPLLI I AEDVEGEALATLVVNKLRGALQVVAVKAPGFGERRKAMLEDIAILTGGEA I FEDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDY DREKLOERLAKLVGGVAVIHVGAATETEMKEKKDRVEDALNATRAAVEEGIVPGGGTAFV RSIKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNA 1 MASKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEI ELEDKFENMGAQMVKEVAPKTSDIAGDGTTTATVLAQAIYREGVKLVAAGRNPMAIKRGI 1 MASKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEI ELEDKFENMGAQMVKEVAPKTSDIAGDGTTTATVLAQAIYREGVKLVAAGRNPMAIKRGI Gaps 0 Indels Matches 548; Conservative 548 MGGMDGMY 61 61 121 121 181 241 301 361 361 421 481 481 541 à g à g ò g ò g Q g ð a G à g à Db ð a ð

describes Streptococcal Hsps, designated Hsp60. These proteins, their fragments, variants and fusion proteins, are used to elicit or enhance an immune response against Streptococcus, and to elicit a similar response to a target antigen fused to the protein. Unlike other immunological carriers, Hsp60 proteins are not immunosuppressive so provide an increased response to any conjugated or fused antigen. Also, where used for cancer control, they lack the side effects associated where used for cancer control, they lack the side effects associated where used for cancer control, they lack the side effects associated with endocoxins. They can also be used to detect specific antibodies and in treatment or prevention of tumours (e.g. sarcoma or cancers of pracast, ovary, prostate, lung, pancreas or liver). The Hsp60 protein is source of primers and probes for detecting streptococci in standard hybridization/amplification assays, and therapeutically in gene EDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDYDR 362 EDKFENMGAQMVKEVAPKTSDIAGDGTTTATVLAQAIYREGVKLVAAGRNPMAIKRGIDK 122 AVVAVTKELSDITKPTRDQKEIAQVGTISANSDTTIGNIIAEAMAKVGKGGVITVEEAKG 182 122 AVDAVVEELKATAKPVETKEEIAQVATISANGDEEIGELIAEAMEKVGKEGVITVEEGKT 3 SKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEIEL 183 LETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQVAK 243 VNRPLLIIAEDVEGEALATLVVNKLRGALQVVAVKAPGFGERRKAMLEDIAILTGGEAIF Gaps 7; DB 20; Length 85; Indels Score 1864.5; DB 20 Pred. No. 1.1e-114; 68.9%; Scor. 69.6%; Pred. No. 1.1. '-- 74; Mismatches 380; Conservative Local Similarity 545 AA; therapy vectors. Sequence 62 303 Query Match 63 123 Matches 8 δ 셤 g ð q à 엄 ò 480 540 180 120 120 240 300 360

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242

AAY23930 standard; Protein; 545

RESULT 2

MGGMDGMY

22-SEP-1999 (first entry)

XHXK

AAY23930;

181

121

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01-JUL-1999;
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                                                                             421 APALDKLKTENGDEATGVNIVLRALEAPLRQIAENAGLEGSVVVEKVKNSEAG-GYNAAT 479
                                                                                                                        GEYEDLIKAGVIDPKKVTRIALQNAASVASLLLTTECAIAEKPEPKKDMP--MPG--GGM 538
                                                                                                                                          GEYVDMIAAGIIDPTKVTRSALQNAASVASLMLTTEAVVVDKPE-KEAAPAGMPGMMGGM 538
EKLOERLAKLVGGVAVIHVGAATETEMKEKKDRVEDALNATRAAVEEGIVPGGGTAFVRS 422
                                                             IKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNAAS 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY23905-30 represent heat shock proteins (Hsps). The specification describes Streptococcal Hsps, designated Hsp60. These proteins, their fragments, variants and fusion proteins, are used to elicit or enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an immune response against Exceptococcus, and to elicit a similar response to a target antigen fused to the protein. Unlike other immunological carriers, Hsp60 proteins are not immunosuppressive so provide an increased response to any conjugated or fused antigen. Also where used for cancer control, they lack the side effects associated with endotoxins. They can also be used to detect specific antibodies and in treatment or prevention of tumours (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or liver). The Hsp60 polynucleotide is used for recombinant production of the protein, as a source of primers and probes for detecting streptococci in standard hybridization/amplification assays, and therapeutically in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid encoding heat shock protein-60 from Streptococcus, ul in vaccines, as carriers for other immunogens, as anticancer
                                                                                                                                                                                                                                                                                                                                                                                                                     Heat shock protein; Hsp; immune response; immunological carrier;
                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer control; tumour; sarcoma; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of a heat shock protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 10A-E; 176pp; English.
                                                                                                                                                                                                                                                                                              AAY23909 standard, Protein; 549 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mizzen L, Wisniewski J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Legionella pneumophila
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62
                            61
                                                                           422 OKALDSLKGDNDDQNMGINILRRAIESPWRQIVTNAGYEASVVVNKVAEHKDNYGFNAAT
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3 SKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEIEL
                 123 AVVAVTKELSDITKPTRDOKEIAQVGTISANSDTTIGNIIAEAMAKVGKGGVITVEEAKG
                                                                                                                                      183 LETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQVAK
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                                                                                                                                                                                                                                                                                                     EDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDYDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa, chitinase, groEL, chiA, antigen; vaccine, diagnosis, detection; infection; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peek K, Sizer PJH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seudomonas aeruginosa groEL protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB69060 standard; Protein; 547 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thompson SE, Smith MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUL-2000; 2000WO-GB02554.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa.
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Antigenic Pseudomonas aeruginosa proteins, useful in the detection

ü

Gaps

7

Length 549; Indels

68.2%; Score 1848; DB 20; 67.3%; Pred. No. 1.4e-113; ative 80; Mismatches 96;

Query Match
Best Local Similarity 67.34
Matches 367; Conservative

pneumophila HtpB gene product.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSIKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNA 480
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                                                                                                                                                                                                                                                                                                                                                                         09
                                                                                                                                                         inducing an immune response against P. aeruginosa infection. An agent capable of antagonising, inhibiting or otherwise interfering with the function or expression of Pl are useful in the manufacture of a medicament for the treatment or prophylaxis of P. aeruginosa infections. The present sequence represents a specifically claimed P. aeruginosa groEL protein sequence from the present invention.
 P. aeruginosa infections and for producing vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKAVVAVTKELSDITKPTRDQKEIAQVGTISANSDTTIGNIIAEAMAKVGKGGVITVEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 DKÁTVÁIVAQLKELAKPCADTKAIAQVGTISANSDESIGQIIAEAMEKVGKEGVITVEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 SGLENELSVVEGMOFDRGYLSPYFVNKPDTMAAELDSPLLLLVDKKISNIREMLPVLEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKVNRPLL11AEDVEGEALATLVVNKLRGALQVVAVKAPGFGERRKAMLED1A1LTGGEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins (PI). The P. aeruginosa proteins have antibacterial activity and can be used in vaccines and as antagonists. The proteins or their fragments, or antibodies are useful in the detection and/or diagnosis of P. aeruginosa. They are also useful for producing a vaccine and
                                                                                                                                                                                                                                                                                                                                                                                        ELEDKFENMGAQMVKEVAPKTSDIAGDGTTTATVLAQAIYREGVKLVAAGRNPMAIKRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGLETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQV
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                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                               The present invention describes antigenic Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                        67.4%; Score 1825.5; DB 22; Length 547; 66.8%; Pred. No. 4.3e-112; ive 75; Mismatches 102; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 547
                                             Claim 3; Fig 25; 129pp; English.
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(first entry)
                                                                                                                                                                                                                                                                                                                       Local Similarity 66.8%
Les 367; Conservative
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 diagnosis of
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                                                                                                                                                                                                                                                                         547 AA;
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22-JUN-1995
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and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDYDR 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDKFENMGAQMVKEVAPKTSDIAGDGTTTATVLAQAIYREGVKLVAAGRNPMAIKRGIDK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 AVVAVTKELSDITKPTRDQKEIAQVGTISANSDTTIGNIIAEAMAKVGKGGVITVEEAKG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQVAK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 VNRPLLIIAEDVEGEALATLVVNKLRGALQVVAVKAPGFGERRKAMLEDIAILTGGEAIF 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 SGRPILIIAEDIEGEALATLVVNNNRGIVKVCAVKAPGFGDRRKAMLQDIAILIKGQVIS 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence of the Helicobacter pylori heat shock protein A (given in AAR67374) was compared to that of other GroEL-like proteins from Legionella pneumophila (AAR67381), Escherichia coli (AAR67382), Chlamydia psittaci (AAR67383), Mycobacterium leprae (AAR67384) and human mitochondrial protein Pl (AAR67385), and regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 SKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 AKELRFGDDARLOMLAGVNALADAVQVTMGPRGRNVVLEKSYGAPTVTKDGVSVAKEIEF
                             Urease; immunogen; vaccine; diagnostic; heat shock protein; HSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.2%; Score 1820.5; DB 16; Length 547; 66.6%; Pred. No. 9.1e-112; ive 82; Mismatches 97; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                                                                                          develop prods. for detection, treatment and prevention of
Helicobacter infection
                                                                                                                                                                                                                                                                                                                                                             DNA from Helicobacter pylori and Helicobacter felis
                                                                                                                                                                                                                                                                                                  ņ
                                                                                                                                                                                                                                                                                                Thiberge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig. 7A(i-vii); 168pp; English.
                                            GroEL-like protein; Helicobacter felis
                                                                                                                                                                                                                                                    (INRM ) INST NAT SANTE & RECH MEDICALE
                                                                                                                                                                                                                                                                                                  Suerbaum S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homology were identified.
                                                                                                                                                                                                     93EP-0401309
93WO-EP03259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363; Conservative
                                                                                                                                                                                                                                                                                                  Ferrero R, Labigne A,
                                                                           Legionella pneumophila
                                                                                                                                                                                                                                                                  (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                               WPI; 1995-006797/01
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                                                                                                           WO9426901-A1
                                                                                                                                                                        19-MAY-1994;
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                                                                                                                                        24-NOV-1994
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RESULT 6 AAB6906:

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241 AKVNRPLLIIAEDVEGEALATLVVNKLRGALQVVAVKAPGFGERRKAMLEDIAILTGGEA 300
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                                                                                                                                            AAV23905-30 represent heat shock proteins (Hsps). The specification describes Streptococcal Hsps, designated Hsp60. These proteins, their fragments, variants and fusion proteins, are used to elicit or enhance
                                             DKAVVAVTKELSDITKPTRDQKEIAQVGTISANSDTTIGNIIAEAMAKVGKGGVITVEEA
                                                                                151 DKATVAIVAQLKELAKPCADTKAIAQVGTISANSDESIGQIIAEAMEKVGKEGVITVEEG
                                                                                                                     181 KGLETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQV
                                                                                                                                                                                                                                                                      I FEDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding heat shock protein-60 from Streptococcus, useful in vaccines, as carriers for other immunogens, as anticancer agents and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heat shock protein; Hsp; immune response; immunological carrier;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer control; tumour; sarcoma; cancer; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of a heat shock protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY23915 standard; Protein; 545 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               567 MGGMGGM 573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-DEC-1997;
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QKALDSLKGDNDDQNMGINILRRAIESPMRQIVTNAGYEASVVVNKVAEHKDNYGFNAAT 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          function or expression of Pl are useful in the manufacture of a medicament for the treatment or prophylaxis of P. aeruginosa infections. The present sequence represents a specifically claimed plrcHisB expression vector groEL fusion protein sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigenic Pseudomonas aeruginosa proteins, useful in the detection and/or diagnosis of P. aeruginosa infections and for producing vaccines
                                                            481 GEYGDWVEMGILDPTKVTRMALQNAASVASLMLTTECMVADL--PKKEEGYGAGDMGGMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilkinson MC;
                                     GEYEDLIKAGVIDPKKVTRIALQNAASVASLLLTTECAIAEKPEPKKDMPMPGGGMGGMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes antigenic Pseudomonas aeruginosa proteins (PI). The P. aeruginosa proteins have antibacterial activity and can be used in vaccines and as antagonists. The proteins or their fragments, or antibodies are useful in the detection and/or diagnosis of P. aeruginosa. They are also useful for producing a vaccine and inducing an immune response against P. aeruginosa infection. An agent capable of antagonising, inhibiting or otherwise interfering with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MASKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEI
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                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa; chitinase; groEL; chiA; antigen; vaccine; diagnosis; detection; infection; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                            pTrcHisB expression vector groEL fusion protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sizer PJH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.2%; Score 1819; DB 22;
66.7%; Pred. No. 1.2e-111;
ive 75; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith MW, Peek K,
                                                                                                                                                                                                                                              AAB69061 standard; Protein; 574 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Fig 26; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99GB-0015419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUL-2000; 2000WO-GB02554.
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Best Local Similarity 66.7%;
                                                                                                                                                                                                                                                                                                                           entry)
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                                                                                                               GMDGM
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                                                                                                                                                                                                                                                                                                                         18-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 ASGEYEDLIKAGVIDPKKVTRIALQNAASVASLLLTTECAIAEKPEPKKUMPMFGGGMGG 540
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an immune response against Streptococcus, and to elicit a similar response to a target antigen fused to the protein. Unlike other immunological carriers, Hsp60 proteins are not immunosuppressive so provide an increased response to any conjugated or fused antigen. Also, where used for cancer control, they lack the side effects associated with endotoxins. They can also be used to detect specific antibodies and in treatment or prevention of tumours (e.g. sarcona or cancers of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ELEDKFENMGAQMVKEVAPKTSDIAGDGTTTATVLAQAIYREGVKLVAAGRNPMAIKRGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSIKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNA
                                                                                                                                          breast, ovary, prostate, lung, pancreas or liver). The Hsp60 polynucleotide is used for recombinant production of the protein, as a source of primers and probes for detecting streptococci in standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIVAEGMKYVTAGMNPTDLKRGI
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                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAAKDVQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVVVDRAFGGPHITKDGVTVAKEI
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                                                                                                                                                                                                         hybridization/amplification assays, and therapeutically in gene
                                                                                                                                                                                                                                                                                                           DB 20; Length 545;
                                                                                                                                                                                                                                                                                                         67.0%; Score 1814.5; DB 20; Lengtl
66.7%; Pred. No. 2.2e-111;
ive 77; Mismatches 103; Indels
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                                                                                                                                                                                                                                                                                                                                                     363; Conservative
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Best Local Similarity
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Scarselli Mora M;

Masignani V, Scalato E, S

Hickey E, Ratti G,

Grandi G, Rappuoli R,

Pizza M, I Venter JC; Galeotti C,

Petersen J, Tettelin H,

Fraser C,

WPI; 2000-062150/05.

N-PSDB; AAZ54509

98US-0098994. 98US-0103749.

31-JUL-1998; 02-SEP-1998;

02-SEP-1998 09-OCT-1998 09-OCT-1998 99US-0121528

09-OCT-1998

INST GENOMIC RES

CHIRON

(CHIR) (GENO-)

98US-0103796

98US-0083758.

99WO-US09346

30-APR-1999;

11-NOV-11999

Neisseria meningitidis.

W09957280-A2

Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics

Claim 2; Page 1388; 1453pp; English.

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represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypoptides. AAE54577 to AAE5455, and AAE4653 to AAE54591 belower polypoptides. AAE54577 to AAE54576 and AAE54613 represent polypoptides. AAE54573 to AAE54576 and AAE54613 represent primers used in the exemplification of the present invention. The polypoptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also he used to screen for agonists or attagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention
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241 AKASRPLLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGBRRKAMLQDIAILIGGTV 300
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Best Local Similarity 66.5
Matches 362; Conservative
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Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.

Neisseria meningitidis ORF 982 protein sequence SEQ ID NO:2966

21-MAR-2000 AAY75747;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae lineticion, this may be in the form of a vaccine or gene therapy. Sequences given in records ABPR1046 represent nucleic acid molecules of the invention.
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             DREKLOERLAKLVGGVAVIHVGAATETEMKEKKDRVEDALNATRAAVEEGIVPGGGTAFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New protein from Neisseria gonorrheae, useful for the manufact
medicament for treating or preventing N. gonorrheae infection
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66.4%; Pred. No. 8.8e-111;
ive 78; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                               Antibacterial; infection; vaccine; gene therapy
                                                                                                                                                                                                                                                                                                                          N. gonorrhoeae amino acid sequence SEQ ID 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Masignani V,
                                                                                                                                                                                                                                                        ABP77245 standard; Protein; 544 AA.
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                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                     Neisseria gonorrhoeae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-058415/05.
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hes 361;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Heat shock protein; hsp60; GroEL protein; therapy; infection; antibiotic.
                                                                                                                                                                                                                                                     61 BLKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIVAEGMKYVTAGMNPTDLKRGI
                                                                                                        KGLETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQV
                                                                                                                              ASGEYEDLIKAGVIDPKKVTRIALQNAASVASLLLTTECAIAEKPEPKKDMPMPGGGMGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polypeptide comprising a component of heat shock protein, Hsp60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                obtainable from Francisella tularensis, useful for preventing or
treating infection caused by Francisella tularensis in an animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sjoestedt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mack KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Francisella tularensis GroEL protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
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The invention relates to a polypeptide comprising at least one

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Conservative

Best Loca Matches

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component of an heat shock protein 60 (hsp60) obtainable from Francisella tularensis, and in particular the GroEL protein or its fragment, and a nucleic acid sequence encoding the polypeptide. The polypeptide and polynucleotides of the invention are useful for preparing a medicament and for preventing or treating infection caused by F. tularensis in an animal. The polynucleotide of the invention is administered to an animal in a form in which it is expressed in situ. The present sequence is Francisella tularensis
                                                                                                                                                                                                                                               65.3%; Score 1769.5; DB 23; Length 544; 64.9%; Pred. No. 2.1e-108; ive 77; Mismatches 113; Indels 1;
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                                                                                                                                                                                                           544 AA;
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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polymoteotides and polypeptides. AAZ54537 to AAZ54556 and AAZ54616 to AAZ545473 represent PCR primers used in the exemplification of the present invention. The

Novel Neisserial polypeptides predicted to be useful antigens for

Claim 2; Page 1385; 1453pp; English.

vaccines and diagnostics

N-PSDB; AAZ54507

Scarselli M;

Masignani V, Mora M; Scalato E, Scarselli

Hickey E, Ratti G,

Galeotti C, Grandi G, , Pizza M, Rappuoli R,

Petersen J, Pizza M, 1 Tettelin H, Venter JC; WPI; 2000-062150/05.

Fraser C,

CHIRON CORP. INST GENOMIC RES.

CHIR GENO-)

98US-0083758. 98US-0098994 98US-0103749 98US-0103796

WO9957280-A2

11-NOV-11999

30-APR-1999;

98US-0099062 98US-0103794 99US-0121528

02-SEP-1998 02-SEP-1998

09-OCT-1998; 09-OCT-1998; 09-OCT-1998;

25-FEB-1999

polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antiboacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.

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                                                                                                                                                                                                                                                                                                                                                                                        78; Mismatches 112; Indels
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Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;

antibacterial; gene therapy.

Neisseria gonorrheae

Neisseria gonorrheae ORF 982 protein sequence SEQ ID NO:2962.

21-MAR-2000

AAY75745;

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08-FEB-2001
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               DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a protein that acts as a detrimental organism controller and is isolated from Enterobacter aerogenes. The invention encompasses a detrimental organism-resistant plant producing the protein of the invention in an effective amount for controlling detrimental organisms. A composition of the invention is useful for the preparation of a detrimental organism controller. The current sequence represents a detrimental organism controller protein of the invention.
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                                                ASGEYEDLIKAGVIDPKKVTRIALQNAASVASLLLITTECAIAEKPEPKKDMPMPGGGMGG
                                    RSIKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                     novel detrimental organism controller for limiting detrimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.6%; Score 1749; DB 23;
64.8%; Pred. No. 4.6e-107;
live 73; Mismatches 115;
                                                                                                                                                                                                                                             Detrimental organism controller protein #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 41-43; 78pp; Japanese.
                                                                                                                                                                                    ABB99014 standard; protein; 545 AA
                                                                                                                                                                                                                                                                 Detrimental organism; enterobacter
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Matches 354;
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                                                                                                                              421 RVASKIADIKGQNEDQNVGIKVALRAMEAPLRQIVINCGEEPSVVANTVKAGDGNYGYNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of a 60 kDa protein from Campylobacter jejuni.
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                                                                                  AVVAVTKELSDITKPTRDQKEIAQVGTISANSDTTIGNIIAEAMAKVGKGGVITVEEAKG
                                                                                                                                             -IKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKD-GFGFNA
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                                             3 SKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEIEL
                                                     EDKFENMGAQMVKEVAPKTSDIAGDGTTTATVLAQAIYREGVKLVAAGRNPMAIKRGIDK
                                                                                                                                     LETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQVAK
                                                                                                                                                                                                 EDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDYDR
                                                                                                                                                                                                                                                                                                                                                                                                                                    Chaperone, GroEL, apical region, disease; protein structure,
Alzheimer's disease, reconditioning; purification, inactivation,
denaturation, therapeutic.
                               . 9
                Length 545;
                64.5%; Score 1746; DB 21;
                              80; Mismatches 108;
                       Pred. No. 7.3e-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/label= GroEL
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                       64.5%;
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               Query Match
Best Local Similarity 64.5
Matches 353; Conservative
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This sequence represents the E. coli chaperone protein GroEL which can be used for treating diseases associated with protein/polypeptide structure, e.g. Alzheimer's disease. The sequence can also be used for reconditioning molecules, especially a protein that has previously been inactivated or denatured, or more generally for altering the structure of a molecule by unfolding or refolding. The sequence also has applications for purification procedures and can increase yield, specific activity or quality of biological molecules, especially by co-expression with the molecules. Therapeutic agents are administered orally, by injection or intranasally, or from a slow-release formulation.
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                                                                                                                                                                                                                                                                                   New chaperone polypeptide(s) derived from GroEL - useful for, e.g. refolding of proteins and for treating diseases associated with protein structure such as Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.5%; Score 1746; DB 19; Length 548; 64.5%; Pred. No. 7.3e-107; Live 74; Mismatches 117; Indels 4
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96WO-GB02980
                                     96GB-0020243
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Best Local Similarity 64.5
Matches 354; Conservative
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                                     26-SEP-1996;
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180

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360

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The invention provides a method of providing chaperone activity in vivo, by administering to a cell a fragment of a molecular chaperone which has in vivo activity. Also provided is a method of determining whether a fragment of a molecular chaperone is active in vivo by: (i) providing a cell with a deficient molecular chaperone activity; (ii) administering the fragment to the cell; and (iii) determining whether the fragment complements the deficient endogenous molecular chaperone. The method can determine which fragments of the molecular chaperone can be used to complement a mutant or deficient molecular chaperone in vivo. The method allows an in vivo assessment of chaperone activity as compared to previous tests which only measured activity in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for, e.g. complementing a molecular chaperone defect in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                            In vivo assay for the detection of chaperone fragment activity
                                                                                                                                             Chaperone; molecular chaperone; groEL gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 52-55; 64pp; English.
             AAW95001 standard; Protein; 548 AA
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                                                                                                             WO9902989 Seq ID 10
                                                                                                                                                                              Escherichia coli
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AAW95001
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2; 120 120 DKAVVAVTKELSDITKPTRDQKEIAQVGTISANSDTTIGNIIAEAMAKVGKGGVITVEEA 180 241 AKVNRPLLIIAEDVEGEALATLVVNKLRGALQVVAVKAPGFGERRKAMLEDIAILTGGEA 300 301 IFEDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDY 360 9 9 BLEDKFENMGAQMVKEVASKANDAAGDGTTTATVLAQAIITEGLKAVAAGMNPMDLKRGI 1 MASKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEI ELEDKFENMGAQMVKEVAPKTSDIAGDGTTTATVLAQAIYREGVKLVAAGRNPMAIKRGI 181 KGLETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQV Gaps 4. Length 548; Indels 64.5%; Score 1746; DB 20; 64.5%; Pred. No. 7.3e-107; tive 74; Mismatches 117; Best Local Similarity 64.58 Matches 354; Conservative 548 AA; 61 121 181 Sequence Query Match g g à ₹ g ò ð

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DREKLOERLAKLVGGVAVIHVGAATETEMKEKKDRVEDALNATRAAVEEGIVPGGGTAFV
                                                                  361 DREKLOERVAKLAGGVAVIKVGAATEVEMKEKKARVEDALHATRAAVEEGVVAGGGVALI
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OM protein - protein search, using sw model

January 28, 2004, 13:15:00 ; Search time 22 Seconds Run on:

(without alignments) 1053.925 Million cell updates/sec

US-09-077-574A-2

2708 1 MASKEILFDAKAREKLSRGV......KDMPMPGGGMGGMGGMDGMY 548 Perfect score:

Seguence:

BLOSUM62 Scoring table:

328717 seqs, 42310858 residues Gapop 10.0 , Gapext 0.5 Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

1: /cgr2 6/ptodata/l/iaa/5A COMB.pep:*
2: /cgn2_6/ptodata/l/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/l/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/l/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/l/iaa/PCTUS COMB.pep:*
6: /cgn2_6/ptodata/l/iaa/PCTUS COMB.pep:* Issued_Patents AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	31,	Sequence 31,	Sequence 31,	209 Sequence	Sequence	Sequence 32,		Sequence 32,	Sequence 32,	9	9	. 9	equence 1,	Seguence 7,	Sequence 33,	Sequence	33,	7	7	η,	Sequence 2,	53 Sequence 153	Sequence 30	Sequence 30	Seguence 30	Sequence 51,	0 Sequence
OLIMATAR	-08-467-822-	-08-432-697-3	-08 - 46	-09-252-991A-	352-5	822-3	US-09-472-971-3	-432-	US-08-466-248-32	-08-470-	US-08-471-491-6	US-08-466-662-6	US-08-256-847C-1	-256-	US-08-467-822-33	US-08-432-697-33	-466	US-08-461-722-2	US-08-336-251-2	US-09-468-041-2	PCT-US94-06362-2	US-09-198-452A-1	-467-822-	US-08-432-697-30	US-08-466-248-30	-09-613-303-5	- 1
Length DB	548 2	548 3	548 3	551 4	550 4	548 2	548 3	548 3	548 3	546 3	546 3	546 3	546 4	546 4	544 2	544 3	544 3	547 4	547 4	547 4	547 5	544 4	545 2	545 3	545 3	641 4	541 2
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Score	84	1844	1844	1820.5	1768.5	1741	1741	1741	1741	1723.5	1723.5	1723.5	1723.5	7	1721	1721		1716.5	1716.5	1716.5	1716.5	70	1702	1702	1702	1683.5	σ O
Result No.	1	01	m	4	5	9	7	00	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

		Sequence 160, App	Sequence 160, App	Sequence 4, Appli	Sequence 17, Appl	Sequence 29, Appl	21,	4	4	4	4	47		19,	34,	34	20
US~08-997-362-160	US-U9-U95-855-160	US-09-324-542-160	US-09-205-426-160	US-09-613-303-4	US-09-613-303-17	US-09-613-303-29	US-09-613-303-21	US-08-461-722-4	US~08-336-251-4	US-09-468-041-4	PCT-US94-06362-4	US-09-134-001C-4705	US-08-467-822-34	US-08-447-154-19	US-08-432-697-34	US-08-466-248-34	US-08-368-834-20
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59.0	0.60	0.69	29.0	58.9	58.9	58.9	58.9	58.8	58.8	58.8	58.8	58.4	58.3	58.3	58.3	58.3	58.2
1597	1001	1587	1597	1595.5	1595.5	1595.5	1595.5	1591.5	1591.5	1591.5	1591.5	1582.5	1577.5	1577.5	1577.5	1577.5	1575
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ALIGNMENTS

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APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Perrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W. CITY: Mashington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/467,822
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 06-JUN-1995
CIASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
                         Sequence 31, Application US/08467822
Patent No. 5843460
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 548 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20005-3315
US-08-467-822-31
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; Sequence 31, Application US/08466248
; Patent No. 6258359
                                                                                                                                                                                                                                                              : 548 amino acids
amino acid
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                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                     FILING DATE: 0:
CLASSIFICATION:
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US-08-466-248-31
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APPLICANT: Ferrero, Richard L.
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: INMUNOSENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEFTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
NUMBER OF SEQUENCES: 44
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                                                                           DB 2;
                                                                           ; Score 1844; DB 2,
; Pred. No. 1e-152;
81; Mismatches 96
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Patent No. 6248330
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1300 I Street, N.W. CITY: Washington
                                                                           68.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Labigne, Agnes
                                                                                                            Matches 366; Conservative
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COMPUTER READABLE FORM:
STRANDEDNESS: single TOPOLOGY: linear
              TOPOLOGY: linear; MOLECULE TYPE: protein US-08-467-822-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
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                                                                                            Best Local Similarity
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US-08-432-697-31
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243 VNRPLLIIAEDVEGEALATLVVNKIRGALQVVAVKAPGFGERRKAMLEDIAILTGGEAIF 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 AVVAVTKELSDITKPTRDQKEIAQVGTISANSDTTIGNIIAEAMAKVGKGGVITVEEAKG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 LETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQVAK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 EDKFENMGAQMVKEVAPKTSDIAGDGTTTATVLAQAIYREGVKLVAAGRNPMAIKRGIDK 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.1%; Score 1844; DB 3; Length 5 67.2%; Pred. No. 1e-152; ive 81; Mismatches 96; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURS SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
EFFRENCE/DOCKET NUMBER: 03495.0137-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                             CUCRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,697
FILING DATE: 02-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 31:
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                         423 IKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNAAS 482
                                                                                                                                                                                                                                   542
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                                       EDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDYDR 362
                                                                              EEIGKSLEGATLEDLGSAKRIVVTKENTTIIDGEGKATEINARIAQIRAQMEETTSDYDR 361
                                                                                                                                                  242 SGRPLLIIAEDIEGEALATLVVNNMRGIVKVCAVKAPGFGDRRKAMLQDIAILTKGQVIS 301
                                                                                                                          EKLQERLAKLVGGVAVIHVGAATETEMKEKKDRVEDALNATRAAVEEGIVPGGGTAFVRS 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MASKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.2%; Score 1820.5; DB 4; 66.7%; Pred. No. 1.2e-150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

FRIOR APPLICATION NUMBER: US 60/074,788

FRIOR FILING DATE: 1998-02-18

FRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 24209, Application US/09252991A; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 543 GMDGM 547
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Matches 36
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                                                                 APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 EDKFENMGAQMVKEVAPKTSDIAGDGTTTATVLAQAIYREGVKLVAAGRNPMAIKRGIDK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 AVVAVTKELSDITKPTRDQKEIAQVGTISANSDTTIGNIIAEAMAKVGKGGVITVEEAKG 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 AVLAVTKKLQAMSKPCKDSKAIAQVGTISANSDEAIGAIIAEAMEKVGKEGVITVEDGNG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 VNRPLLIIAEDVEGEALATLVVNKLRGALQVVAVKAPGFGERRKAMLEDIAILTGGEAIF 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.1%; Score 1844; DB 3; Length 548; 67.2%; Pred. No. 1e-152; live 81; Mismatches 96; Indels
                                                                                                                                                                                                                      Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/466,248
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
                            Sauerbaum, Sebastien
Ferrero, Richard L.
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE, DOCKET NUMBER: 03.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                             1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4000
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
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             Agnes
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Matches 366; Conservative
                                                                                                                                                                                              CORRESPONDENCE ADDRESS: ADDRESSE: Finnegan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                            Sauerbaum,
                                                                                                                                                                          NUMBER OF SEQUENCES;
                                                                                                                                                                                                                                       ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                 Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 06
CLASSIFICATION:
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                            APPLICANT:
                                             APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                               STREET:
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        APPLICANT
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	Ferrero, Ri Thiberge, J Thiberge, J WENTION: HE WENTION: DO VEENTION: CO VEENTION: CO VEENTION: CO SECURNCES: 4 SECURNCES:	APPLICATION NUMBER: US/08/467,822 FILING DATE: 06-JUN-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/447,177 FILING DATE: 19-MAY-1995 CLASSIFICATION NUMBER: US 08/432,697 FILING DATE: 02-MAY-1995 CLASSIFICATION NUMBER: US 08/432,697 FILING DATE: 02-MAY-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: MEYERS. KENNELT US REFERENCE/DOCKET NUMBER: 03495.0137-02000 TELEPRAN: (202) 408-4400	SEQUENCE CHARALEKALEKALICAS
OY 361 DREKLOBRLAKLVGGVAVIHVGRAIFITEMKEKKDRVEDALNATRAAVEEGIVPGGGTAFV 420	RESULT 5 US-09-328-352-5508 US-09-328-352-5508 Sequence 5508, Application US/09328352 Sequence 5508, Application US/09328352 Sequence 5508, Application US/09328352 GENERAL INFORMATION: PAPPLICANT: GARY L. Breton et al. TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION NUMBER: US/09/328,352 CURRENT APPLICATION NUMBER: US/09/328,352 CURRENT FILING DATE: 1999-06-04 SEQ ID NOS: 8252 TURES FRY TYPER FRY TYPER FRY TYPER FRY US-09-328-352-5508	Query Match 65.3%; Score 1768.5; DB 4; Length 550; Best Local Similarity 64.0%; Pred. No. 4.1e-146; Indels 1; Gaps 1; Matches 348; Conservative 87; Mismatches 108; Indels 1; Gaps 1; QY	241 247 301 301 361 421 421

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APPLICANT: Saucerbaum, Sebastien
APPLICANT: Saucerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiborge, Jean-Michel
TITLE OF INVENTION: IMMINGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
OUNDER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
181 TGLQDELDVVEGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNIREMLPVLEAV 240
                                                                              IFEDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDY 360
                                                                                                                                                        DREKLOERLAKLVGGVAVIHVGAATETEMKEKKDRVEDALNATRAAVEEGIVPGGGTAFV 420
                                                        AKVNRPLLIIAEDVEGEALATLVVNKLRGALQVVAVKAPGFGERRKAMLEDIALLTGGEA 300
                                                                                                                                                                                                                               RSIKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNA
                                                                                                                                                                                                                                                                                                          481 ASGEYEDLIKAGVIDPKKVTRIALQNAASVASLLLTTECAIAEKPEPKKDMPMPG--GGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.30
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ER: 03495.0137-00000
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APPLICATION NUMBER: US/08/432,697
FILING DATE: 02-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 32, Application US/08432697
; Patent No. 6248330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1300 I Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meyers, Kenneth J. REGISTRATION NUMBER: 25,: REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Labigne, Agnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   548 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
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OPERATING SYSTEM:
SOFTWARE: PATENTI
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US-08-432-697-32
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STATE:
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             DKAVVAVTKELSDITKPTRDQKEIAQVGTISANSDTTIGNIIAEAMAKVGKGGVITVEEA 180
                                   KGLETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQV 240
                                                                                                                                                          241 AKVNRPLLIIAEDVEGEALATLVVNKLRGALQVVAVKAPGFGERRKAMLEDIAILTGGEA 300
                                                                                                                                                                                    420
                                                                                                                                                                                                                                                                                                                                                                                      421 RSIKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNA 480
                                                                                                                                                                                                                                                                                                                                                                                                                538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                 TGLQDELDVVEGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNIREMLPVLEAV
                                                                                                                                                                                                                                                                                                                                   301 IFEDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDY
                                                                                                                                                                                                                                                                                                                DREKLOERLAKLVGGVAVIHVGAATETEMKEKKDRVEDALNATRAAVEEGIVPGGGTAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASGEYEDLIKAGVIDPKKVTRIALQNAASVASLLLTTECAIAEKPEPKKDMPMPG--GGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELEDKFENMGAQMVKEVAPKTSDIAGDGTTTATVLAQAIYREGVKLVAAGRNPMAIKRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKAVVAVTKELSDITKPTRDQKEIAQVGTISANSDTTIGNIIAEAMAKVGKGGVITVEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MASKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SOGO, Kazuyo
APPLICANT: YANAGI, Hideki
APPLICANT: YANAGI, Hideki
TITLE OF INVENTION: TRIGGER FACTOR EXPRESSION PLASMIDS
FILE REFERENCE: 1422-409P
CURRENT APPLICATION NUMBER: US/09/472,971
CURRENT APPLICATION NUMBER: US/09/372965
EARLIER APPLICATION NUMBER: JP10-372965
EARLIER APPLICATION NUMBER: JP10-372965
MUMBER OF SEQ ID NOS: 7
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Patent No. 6197547
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US-09-472-971-3
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Matches 353; Conserv
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SOFTWARE: Pater.
SEQ ID NO 3
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APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
NUMBER OF SEQUENCES: 44
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                                                                                                                                                                                    ELEDKFENMGAQMVKEVAPKTSDIAGDGTTTATVLAQAIYREGVKLVAAGRNPMAIKRGI 120
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                                                                                                                                                                                                          61 ELEDKFENMGAQMVKEVASKANDAAGDGTTTATVLAQALITEGLKAVAAGMNPMDLKRGI
                                                                                                                              1 MASKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEI
                                                                       Gaps
                                                                       4.
                             64.3%; Score 1741; DB 3; Length 548;
64.3%; Pred. No. 1e-143;
tive 74; Mismatches 118; Indels
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Dunner
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 32, Application US/08466248
Patent No. 6258359
GENERAL INFORMATION:
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                                                                           353; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         539 GGMGGMDGM 547
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                                     Query Match
Best Local Similarity
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STATE: D.C
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US-08-466-248-32
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US-08-432-697-32
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481 ASGEYEDLIKAGVIDPKKVTRIALQNAASVASILLITTECAIAEKPEPKKDMPMPG--GGM 538
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Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                              03495.0137-02000
                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                              JMBER: US/08/466,248
06-JUN-1995
                                                          FILING DATE: 06-UUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NORTH:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                           NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146;
REFERENCE/DOCKET NUMBER: 0349;
TELECOMMUNICATION INFORMATION:
TELEPAN: (202) 408-400
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 548 amino acids
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                       CURRENT APPLICATION DATA:
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                                              APPLICATION NUMBER:
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EDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDYDR 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
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ORGANISM: Helicobacter pylori
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Matches 350; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BGKPLLIIAEDIEGEALTTLVVNKLRGVLNIAAVKAPGFGDRRKEMLKDIAILTGGQVIS 301
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                                                                                                                                                                                                   Helicobacter Pylori Proteins Useful for Vaccines and Diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0316.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
TELEPHONE: (510) 661-2708
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,848
FILING DATE: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                Sequence 6, Application US/08470260
Patent No. 6077706
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           Chiron Corporation
                                                                                                         Antonello
                                                                                                     APPLICANT: Covacci, Antonella
APPLICANT: Bugnoli, Massimo
APPLICANT: Telford, John
APPLICANT: Macchia, Giovanni
APPLICANT: Rappuoli, Rino
                                                                                                                                                                                                                                                                                               4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 64.1%,
Matches 350; Conservative
                                                                                                                                                                                 Rappuoli, Rino
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                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94608-2916
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                CITY: Emeryville STATE: California
                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                        USA
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             RESULT 10
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                                                                                                                                           362 EKLOERLAKLSGGVAVIKVGAASEVEMKEKKORVDDALSATKAAVEEGIVIGGGAALIRA 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Covacci, Antonello
APPLICANT: Bugnonli, Massimo
APPLICANT: Telford, John
APPLICANT: Macchia, Giovanni
APPLICANT: Rappuoli, Rino
TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And
TITLE OF INVENTION: Diagnostics
FILE REFERENCE: CHIRO044
                                                                                                                                                                                                                                                                                                                                 483 GEYEDLIKAGVIDPKKVTRIALQNAASVASLILLTTECAIAEKPEPKKDMPMPG-GGMGGM
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64.1%; Pred. No. 3.5e-142;
iive 73; Mismatches 120; Indels
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GENERAL INFOGRATION: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
APPLICANT: Costantino, Paolo
APPLICANT: Costantino, Paolo
TTILE OF INVENTION: Conjugates Formed From Heat Shock Proteins And Oligo or Polysacch
FILE REFERENCE: CHIR-0042
CURRENT APPLICATION NUMBER: 105/08/256,847C
CURRENT APPLICATION NUMBER: PCT/EP93/00516
PRIOR FILING DATE: 1993-03-08
PRIOR FILING DATE: 1993-03-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
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422 AQKVH--LNLHDDEKVGYEIIMRAIKAPLAQIAINAGYDGGVVVNEVEKHEGHFGFNASN 479
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                                                                                                                                                                                                                         ; Sequence 1, Application US/08256847C
; Patent No. 6403099
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                                                                                                        GGMDGM 547
                                                                                                                                         540 GGMGGM 545
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ORGANISM: H. pylori
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                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                              RESULT 13
US-08-256-847C-1
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APPLICANT: Covacci, Antonello
APPLICANT: Telforid, John
APPLICANT: Telforid, John
APPLICANT: Macchia, Glovanni
APPLICANT: Rappuoli, Rino
TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And
TITLE OF INVENTION: Diagnostics
                                                                                                                            GEYEDLIKAGVIDPKKVTRIALQNAASVASILLITTECAIAEKPEPKKDMPMPG-GGMGGM
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                                                        423 IKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNAAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.6%; Score 1723.5; DB 3; 64.1%; Pred. No. 3.5e-142; iive 73; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: CHIRODS7
CURRENT APPLICATION NUMBER: US/08/466,662B
CURRENT FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08466662B Patent No. 6130059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
Matches 350; Conserv
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APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INPECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 DKAVKVVVDEIKKISKPVQHHKEIAQVATISANNDABIGNLIAEAMEKVGKNGSITVEEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MASKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.6%; Score 1721; DB 2; Length 59
64.8%; Pred. No. 5.7e-142;
Live 73; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,822
FILING DATE: OG-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                         Sequence 33, Application US/08467822
Patent No. 5843460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Meyers, Kenneth J. REGISTRATION NUMBER: 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 544 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 64.8'
Matches 351; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunner
         540 GGMGGM 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : D.C.
RY: USA
20005-3315
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                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Labion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 0;
CLASSIFICATION:
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                                                                             RESULT 15
US-08-467-822-33
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COUNTRY:
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                                                                                                                                                                                                                                                                        APPLICANT: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
APPLICANT: Costantino, Paolo
APPLICANT: Costantino, Paolo
TITLE APPLICANT: Costantino, Conjugates Formed From Heat Shock Proteins And Oligo or Polysacch
FILE REFERENCE: CHIR-0042
CURRENT APPLICATION WUMBER: US/08/256,847C
CURRENT APPLICATION WUMBER: PCT/EP93/00516
PRIOR APPLICATION NUMBER: PCT/EP93/00516
PRIOR FILING DATE: 1993-03-08
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
480 GKYVDMFKEGIIDPLKVERIALQNAVSVSSLLLTTEATVHEIKEEKATPAMPDMGGMGGM 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCPVANMGAQLVKEVASKTADAAGDGTTTATVLAYSIFKEGLRNITAGANPIEVKRGMDK 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 LETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQVAK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDYDR 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 AAEALINELKKASKKVGGKEEITQVATISANSDHNIGKLIADAMEKVGKDGVITVEEAKG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 VNRPLLIIAEDVEGEALATLVVNKLRGALQVVAVKAPGFGERRKAMLEDIAILTGGEAIF 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKLQERLAKLVGGVAVIHVGAATETEMKEKKDRVEDALNATRAAVEEGIVPGGGTAFVRS 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 IKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNAAS 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 SKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEIEL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AKEIKFSDSARNLLFEGVRQLHDAVKVTMGPRGRNVLIQKSYGAPSITKDGVSVAKEIEL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      483 GEYEDLIKAGVIDPKKVTRIALQNAASVASLLLTTECAIAEKPEPKKDMPMPG-GGMGGM
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; Pred. No. 3.5e-142;
73; Mismatches 120; Indels 3;
                                                                                                                                                                                                              Sequence 7, Application US/08256847C Patent No. 6403099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.6%;
64.1%;
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                                              542 GGMDGM 547
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Best Local Similarity
Matches 350; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: H. pylori
US-08-256-847C-7
                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                      US-08-256-847C-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 546
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301 IFEDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDY 360
                                                          241 AKVNRPLLIIAEDVEGEALATLVVNKIRGALQVVAVKAPGFGERRKAMLEDIALLTGGEA 300
                                 181 KGLETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQV 240
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Search completed: January 28, 2004, 13:18:23 Job time : 24 secs

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(without alignments)
2981.360 Million cell updates/sec
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/cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        777136 segs, 206736638 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Applications AA:*
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                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                          January 28, 2004, 13:17:21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	17524 Seguence 17524.	4	Sequence	Sequence	Seguence	Seguence	Seguence	Seguence	Seguence	Sequence	Sequence	Seguence	Seguence	Semience	Sequence
ΩI	US-10-369-493-17524	US-10-369-493-1001	US-10-369-493-11760	US-10-369-493-7917	US-10-369-493-10295	US-10-369-493-9287	US-10-369-493-15468	US-10-369-493-1	US-10-369-493-1	US-10-369-493-11922	US-10-369-493-1	US-10-369-493-1	US-10-369-493-1	US-10-369-493-167	US-10-369-493-17132
DB	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12
% Query Match Length DB	547	547	544	547	542	541	544	544	543	542	551	540	552	545	544
% Query Match	68.8	9.89	0.89	67.9	67.8	67.7	67.7	67.7	67.5	67.4	6.99	6.99	8.99	0.99	65.7
Score	1862.5	1857	1840.5	1839.5	1835.5	1834	1833	1833	1828.5	1826	1812.5	1811	1810	1786	1780.5
Result No.	1	7	e	4	2	9	7	80	თ	10	11	12	13	14	15

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	Sequence 10, Appl Sequence 23094, A Sequence 10862, Ap Sequence 9597, Ap Sequence 118, App Sequence 181, App Sequence 2, Appli	Sequence 513, App Sequence 513, App Sequence 17907, A Sequence 20184, A Sequence 51, Appl Sequence 51, Appl Sequence 5, Appli Sequence 8322, Appli	11465, 2950, 12526, 20276, 160, Ap 160, Ap
-10-228-167A- -10-369-493-4 -10-369-493-4 -10-369-493-7 -10-192-419-2 -09-415-849-1	US-02-276-455-10 US-10-369-493-23944 US-10-369-493-9597 US-10-369-493-9597 US-09-882-227-418 US-10-369-493-181 US-10-046-649-2	US-10-369-463-513 US-10-289-762-153 US-10-369-493-17907 US-10-369-493-20184 US-10-267-311-51 US-10-369-493-18994 US-10-369-493-8322 US-10-369-493-8322	US-10-156-761-11465 US-10-369-493-2950 US-10-156-761-12526 US-10-369-493-20276 US-08-880-505-160 US-10-205-979-40 US-10-051-643-160 US-09-847-637B-6
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1778.5 1771.5 1770 1770 1746	1746 1743.5 1737.5 1720.5 1716.5	1708.5 1698.5 1698.5 1683.5 1683.5 1658	1636 1628.5 1610.5 1597 1597 1597 1597
16 17 18 19 20 21	2 2 2 2 2 2 2 3 2 4 3 2 4 3 5 4 5 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	

ALIGNMENTS

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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Chen, Manfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
FILE REFERENCE: 38-10(52052)B
FILE REPRENT APPLICATION NUMBER: US, 10/369, 493
FRIOR APPLICATION NUMBER: US, 60/360, 039
FRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ELADKFENMGAQMLKEVASKTNDHAGDGTTTATVLAQALIREGCKAVAAGMNPMDLKRGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.8%; Score 1862.5; DB 12; Length 547; 66.8%; Pred. No. 1.3e-138; Live 80; Mismatches 97; Indels 5;
                      Sequence 17524, Application US/10369493
Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Xylella fastidiosa
US-10-369-493-17524
                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 17524
LENGTH: 547
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                                                                   GENERAL INFORMATION:
US-10-369-493-17524
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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Sequence 11760, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Cao, Yongwei

APPLICANT: Glodman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: VUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-21

PRIOR FILING DATE: 2002-02-21
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                                                                                                                                                                                              DREKLOERLAKLVGGVAVIHVGAATETEMKEKKDRVEDALNATRAAVEEGIVPGGGTAFV 420
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                                                                                                                                       181 KGLETTLDVVEGMQFDRGYLSPYFVTNADKMLVQMENPLILLVEKKISNLQQILQILEGA
                                    241 AKVNRPLLIIAEDVEGEALATLVVNKLRGALQVVAVKAPGFGERRKAMLEDIAILTGGEA
                                                                                                                                                                                                                                                                          421 RSIKV-LDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKD-GFGF
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                                                                                                                  IFEDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDY
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69.2%; Pred. No. 6.9e-137;
live 69; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 11760
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Best Local S
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APPLICANT: Cao, Yongwei
APPLICANT: Binkle, Gregory J.
APPLICANT: Binkle, Greven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Rarression of MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: REPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
THE REPRESSENCE: 38-10/52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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                                               KGLETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQV 240
                                                                                                                           241 AKVNRPLLITAEDVEGEALATLVVNKLRGALQVVAVKAPGFGERRKAMLEDIALLTGGEA 300
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                                                                                                                                                                                                        301 IFEDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDY
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                                                                 TILENELDVVEGMQFDRGYSSPYFINNQQSQIVELDNPYILLHDKKISSVRDLLTVLDAV
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69.5%; Pred. No. 3.4e-138;
tive 72; Mismatches 90;
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PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10014, Application US/10369493 Publication No. US20030233675A1
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Best Local Similarity 69.55
Matches 382; Conservative
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SEQ ID NO 10014
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN FLANTS FOR PRODUCTION OF
FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
FRIOR APPLICATION NUMBER: US 60/360,039
FRIOR FILING DATE: 2002-02-21
                                                                      301 ISEDLGMKLENVTIDMLGRAKKISINKDNTTIVDGNGDKAEIDARVAQIRNQIEETSSDY 360
                                               DREKLØERLAKLVGGVAVIHVGAATETEMKEKKDRVEDALNATRAAVEEGIVPGGGTAFV 420
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; ORGANISM: Cytophaga hutchinsonii
US-10-369-493-10295
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Best Local Similarity
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APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: EXPRISESION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT PAPLICATION NUMBER: US,10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR PHILING DATE: 2003-02-28
PRIOR PHILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 7917
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                                                                                                          361 DREKLQERLAKLVGGVAVIHVGAATETEMKEKKDRVEDALNATRAAVEEGIVPGGCTAFV 420
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241 VQTGKPLVIIAEDVEGEALATLVVNKLRGGLKIAAVKAPGFGDRRKAMLEDIAILTGGTV 300
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                                     I FEDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDY
                                                       421 RSIKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREP-KDGFGFN
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Publication No. US20030233675A1
GENERAL INFORMATION:
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
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Best Local Similarity 67.9%
Matches 372; Conservative
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFRENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PRING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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481 ATGEFGDMVKLGILDPTKVARTALQNAASIAGLMITTEAMVAE--APKKDEPTPPAAGGG
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; Pred. No. 2.7e-136;
82; Mismatches 95;
                                                                                                                                                              ; Sequence 15468, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Xanthomonas campestris
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66.8%;
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Best Local Similarity 66.8<sup>†</sup>
Matches 365; Conservative
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION (TITLE OF INVENTION: PLANTS MITH IMPROVED PROPERTIES
FILE REPRENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369, 493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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                                            423 IKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNAAS 482
                                                                    362 EKLQERLAKLSGGVAIMYIGAATEVEMKEKKDRVDDALHATRAAVEEGIVPGGGVALIRA 421
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; Pred. No. 2.2e-136;
80; Mismatches 101;
                                                                                                                                                                                                                                               ; Sequence 9287, Application US/10369493 ; Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.33
Matches 360; Conservative
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-369-493-9287
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TYPE: PRT ORGANISM: Agrobacterium tumefaciens
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Matches 374; Conservative
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                                                                                                APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
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66.8%; Pred. No. 2.7e-136;
iive 82; Mismatches 95;
                                                              Sequence 16217, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Xanthomonas campestris
US-10-369-493-16217
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SEQ ID NO 16217
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Matches 365; Conservative
 539 GGMGGM 544
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RESULT

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APPLICANT: Goo, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPERSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE REPERENCE: 38-10 (52052)8
FILE REPERENCE: 38-10 (52052)8
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 15265
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Sequence 15265, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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8-10-369-493-11922
Sequence 11922, Application US/10369493
Publication No. US20030233675Al
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/369,493
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Publication No. US20030233675A1
                 CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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                                                                                                                                                                                             Query Match
Best Local Similarity 67.8%
Matches 375; Conservative
                                                                       NUMBER OF SEQ ID NOS: 47374
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                                                                                         SEQ ID NO 12330
LENGTH: 551
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APPLICANT: Chen, Xianfeng TITLE OF INVENTION: EXPERSION OF MICROBIAL PROTEINS IN FLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPERSION OF MICROBIAL PROPERTIES
FILE REPERENCE: 38-10(52052) B
                                                                  APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xiaffeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE REPREBENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
FRICA APPLICATION NUMBER: US 60/360,039
PRICA FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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67.8%; Pred. No. 9.5e-136;
17ve 80; Mismatches 92;
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
                                  Hinkle, Gregory J.
Slater, Steven C.
Goldman, Barry S.
Chen, Xianfeng
                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Mesorhizobium loti
                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 67.8
Matches 366; Conservative
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US-10-369-493-12330
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                                                                                                                                                                                                                                          SEQ ID NO 11922
LENGTH: 542
                   APPLICANT: CAPPLICANT: APPLICANT:
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianteng
TITLE OF INVENTION: RIPERSSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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                                                                             1 MASKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEI
                                                                                                          11;
Length 551;
                                         96; Indels
  DB 12;
Score 1812.5; DB 11
Pred. No. 1.1e-134;
66.9%; Score 1512...,
67.8%; Pred. No. 1.1e-
rive 71; Mismatches
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CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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66.08;
    ORGANISM: Mesorhizobium loti
       ; OKGANISM: MESULI
US-10-369-493-12170
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Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: UNMER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
FRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12170
TYPE: PRT
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                                                                                                     DB 12; Length 540;
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                                                                                                                                      95;
                                                                                                  66.9%; Score 1811; DB 12;
66.6%; Pred. No. 1.5e-134;
live 82; Mismatches 95;
                                                        ORGANISM: Xanthomonas campestris
                                                                                                                Local Similaricy ... hes 361; Conservative
NUMBER OF SEQ ID NOS: 47374
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              SEQ ID NO 15838
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERIES
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERIES
FILE REPERENCE: 38-10 (52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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                                                       Gaps
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     Length 552;
                                                       Indels
66.8%; Score 1810; DB 12;
67.6%; Pred. No. 1.8e-134;
iive 72; Mismatches 99;
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; Publication No. US20030233675A1
; GENERAL INFORMATION:
                     Best Local Similarity 67.63
Matches 373; Conservative
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Length 545;

DB 12;

Score 1786;

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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Glodman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REPERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
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                                                                                                                                                                                                                                                                                                                         IFEDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDY 360
                                                                                                ELEDKFENMGAQMVKEVAPKTSDIAGDGTTTATVLAQAIYREGVKLVAAGRNPMAIKRGI 120
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             Indels
No. 1.4e-132;
smatches 86;
                94; Mismatches
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Publication No. US20030233675A1
GENERAL INFORMATION:
 Pred.
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; ORGANISM: Bacillus halodurans
US-10-369-493-17132
 64.9%;
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SEQ ID NO 17132
                Matches 352; Conservative
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Best Local Similarity
Matches 355; Conservat
  Best Local Similarity
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US-10-369-493-17132
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241 QGKPILLIAEDVBGEALATLVVNKLRGTFNAVAVKAPGFGDRRKAMLEDIALLTGGEVIT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNAAS 482
                                                              EDKFENMGAQMVKEVAPKTSDIAGDGTTTATVLAQAIYREGVKLVAAGRNPMAIKRGIDK 122
                                                                                         62 EDAFENMGAKLVAEVASKTNDIAGDGTTTATVLAQAMIREGLKNVTSGANPMVIRKGIEK 121
                                                                                                                                                    AVVAVTKELSDITKPTRDQKEIAQVGTISANSDTTIGNIIAEAMAKVGKGGVITVEEAKG 182
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Search completed: January 28, 2004, 13:22:58
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OM protein - protein search, using sw model

January 28, 2004, 13:11:55 Run on:

; Search time 21 Seconds (without alignments) 2509.545 Million cell updates/sec

US-09-077-574A-2
2708
1 MASKEILFDAKAREKLSRGV......KDMPMPGGGMGGMGGMDGMY 548 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	chaperonin groELX	groEL2 chaperonin	heat shock protein	60kDa chaperonin X	chaperonin GroEL -	60K heat shock pro	heat shock protein	Conf0 protein (Gro	chaperonin 60 - Co		O	60K chaperonin (pr		PA	groEL - Brucella a	sho	shock			chaperonin 60kD su		60K chaperonin gro	chaperonin groEL -	groEL protein - Ba	0	υ,		shock	shock
		OI .	JC2562	C95311	JN0509	F82783	B47073	A41468	865596	140331	S39765	F95967	AD2660	B97442	823918	B83098	S22347	835309	140342	B36917	JN0512	H81964	JC2564	AG3640	S47530	S37039	C81021	B43606	S61300	B54539	S61302
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		Length	551	545	545	547	546	550	546	547	552	542	544	544	544	547	546	550	546	544	541	544	549	546	545	544	544	547	544	546	544
	Query	Match		8.8	8.8	8.8	œ	1.8	8.1	68.1	8.1	8.0	8.0	68.0	7.5	67.4	67.3	7.3	67.3	67.1	67.1	7.0	7.0	7.0	9	6.9	6.8	6.7	9.9	6.4	6.3
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		Score	1866	1864	S	٠,	1852.5	1845	1844.5	1843.5	1843.5	184	1840.5	1840.5	1828.5	1825.5		1823	1822	1817.5	1816.5	814	1814.5	н	812.	1810.5	1808.5	1805.5	1802.5	1799	1794.5
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123 AVVAVTKELSDITKPTRDQKEIAQVGTISANSDTTIGNIIAEAMAKVGKGGVITVEEAKG 182

63 EDKFENMGAQMVKEVAPKTSDIAGDGTTTATVLAQAIYREGVKLVAAGRNPMAIKRGIDK 122

3 SKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEIEL 62

2 AKELRFGDDARQQMLAGVNALADRVKATMGPSGRNVVLERSFGAPTVTKDGVSVAKEIEF

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183 LETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQVAK 242

heat shock cognate	chaperonin, 60 kDa	heat shock protein	heat shock protein	heat shock protein	GroEL - Aquifex ae	chaperonin groEL -	class I heat-shock	heat shock protein	chaperonin froEL -	heat shock protein	chaperonin, 60 Kd	60 kDa chaperonin	chaperonin groEL -	heat shock protein	60 kn changronin (
835311	B87334	S61301	JN0511	S61303	C70489	JC6063	B83720	851563	B43827	S34938	B82048	AG0043	C64076	B49855	G81328
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546 2	547 2	541 2	541 2	544	545	544	544 2	545 2	544 1	546	544 2	548	548 2	539 2	745
	66.2 547 2														
66.2		66.1	66.1	0.99	0.99	65.7	65.7	65.5	65.5	65.2	65.0	65.0	65.0	64.8	64.8

ALIGNMENTS

002562
chaperonin groELx protein - Amoeba proteus
C;Species: Amoeba proteus
C,Date: 17-May-1995 #sequence revision 14-Jul-1995 #text change 26-Aug-1999
C, Accession: JC2562
R;Ahn, T.I.; Lim, S.T.; Leeu, H.K.; Lee, J.E.; Jeon, K.W.
Gene 148[128], 43-49, 1994
A; Title: A novel strong promoter of the groEx operon of symbiotic bacteria in Amoeba prot
A; Reference number: JC2561
A; Note: due to a typographical error the volume number 148 appears as 128
A;Accession: JC2562
A; Molecule type: DNA
A; Residues: 1-551 <ahn></ahn>
A; Cross-references: GB: M86549; NID: q155400; PIDN: AAC09381.1: PID: q155402
C; Comment: This protein is involved in the assembly of oligomeric protein complexes and
C; Genetics:
A; Gene: groELx
C;Superfamily: chaperonin groEL
C;Keywords: molecular chaperone
Undery Mattern 68.9%; Score 1866; DB 2; Length 551;
Matches 3/3; Conservative /4; Mismatches 96; Indels 6; Gaps 2;

61

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A;Title: Cloning and characterization of multiple groEL chaperonin-encoding genes in Rhi A;Reference number: JN0509; MUID:93231539; PMID:8097179
A;Accession: JN0509
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M94192; NID:g152233; PIDN:AAA26285.1; PID:g152235
C;Comment: This protein plays a role in protein folding and in the extracellular transpo
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                                                                                                                                                                                                       DREKLQERLAKLVGGVAVIHVGAATETEMKEKKDRVEDALNATRAAVEEGIVPGGGTAFV 420
                                                                                                                   heat shock protein groEL (clone Rhz A) - Rhizobium meliloti
NyAlternate names: chaperonin groEL protein
C;Species: Rhizobium meliloti
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C;Accession: JND509
R;Rusanganwa, E.; Gupta, R.S.
Gene 126, 67-75, 1993
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                                                                                                                                                                             NAASGEYEDLIKAGVIDPKKVTRIALONAASVASLLLTTECAIAEKPEPKKDMPMPGGGM
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                       R-SIKVLDDIKPADDDELAGLNIRRSLEEPLRQIAANAGYEGSIVVEKVREPK-DGFGF
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C;Superfamily: chaperonin groEL
C;Keywords: heat shock; molecular chaperone; stress-induced protein
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Pred. No. 3e-83;
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Best Local Similarity
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R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows, R.Barnett, M.J.; Fisher, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9893-9888, 2001
A,Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Accession: C95311
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A.Actatus: preliminary
A.Actatus: preliminary
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A.Actatus: preliminary
A.Actatus: preliminary
A.Rosiques: 1-545 <KUR>
A.Cross-references: GB.AE006469; PIDN:AAK65053.1; PID:g14523485; GSPDB:GN00165
A.Experimental source: strain 1021, megaplasmid pSymA
A.Experimental source: strain 1021, megaplasmid pSymA
B.Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
D.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A.Authors: Kahn, M.L.; Kahman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
A.Authors: Kahn, D.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A.Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A.Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                  groEL2 chaperonin [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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                                                          IKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNAAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
A;Gene: groEL2
A;Gene: plasmid
C;Superfamily: chaperonin groEL
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Matches 387; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                chaperonin GroEL - Chromatium vinosum C;Species: Chromatium vinosum C;Species: Chromatium vinosum C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999 C;Accession: B47073

R;Ferreyra, R.G.; Soncini, F.C.; Viale, A.M.
J. Bacteriol. 175, 1514-1523, 1993

A;Title: Cloning, characterization, and functional expression in Escherichia A;Reference number: A47073; MUID:93186721; PMID:8444812
DREKLOERLAKLVGGVAVIHVGAATETEMKEKKDRVEDALNATRAAVEEGIVPGGGTAFV
                       RSIKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNA
                                                                                                                                                                              ASGEYEDLIKAGVIDPKKVTRIALQNAASVASLLLTTECAIAEKPEPKKDMPMP---GGG
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68.2%; Pred. No. 9.7e-83;
ive 70; Mismatches 101; Indels
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Best Local Similarity 68.2%
Matches 374; Conservative
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A;Molecule type: nucleic acid
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                                                                                                                                                                                                                                                          60kDa chaperonin XF0615 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: F82783
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A. Experimental source: strain 9a5c
R. Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; P. Pariones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H. Sabiones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H. Submitted to GenBank, June 2000
A. Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajina, J.P.; Krieger, J.E.; Kuramae, B.E.; Laigr Ghado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F. R.; Oliveira, M.A.; Menos, L.R.; Oliveira, M.R.; Menos, M.C.; de Oliveira, R.C.; Palmieri, D.B. Rodrigues, V.; Rosa, A.J. de M.A.; da Silva, M.R.; da Silva, A.M.; da Silva, A.M.; da Silva, A.M.; da Silva, A.M.; Vallada, H.; Van Sluys, M.A.; Salva, A.M.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zakasak A.Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE003907; GB:AE003849; NID:g9105484; PIDN:AAF83425.1; GSPDB:GN001
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A;Note: for a complete list of authors see reference number A59328 below
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Pred. No. 3.2e-83;
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66.8%;
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C;Superfamily: chaperonin groEL
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Matches 366; Conservative
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A; Molecule type: DNA
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(Species: Rhizobium leguminosarum

(Species: Rhizobium leguminosarum

(Spacession: 865596

(Accession: 865596

Mirrobiology 140, 113-122, 1994

A.Ritle: Rhizobium leguminosarum contains multiple chaperonin (cpn60) genes.

A,Reference number: 865596; MUID:94214663; PMID:7909257

A,Reference number: 865596; MUID:94214663; PMID:7909257
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A;Residues: 1-546 <WAL>
A;Cross-references: EMBL:L20775; NID:g387873; PIDN:AAA26246.1; PID:g387874
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                                                                                                                                                heat shock protein 60 - Rhizobium leguminosarum
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: cpn60
C;Superfamily: chaperonin großL
C;Keywords: heat shock; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.88;
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Best Local Similarity 69.8%
Matches 384; Conservative
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                                                                                                                                                                              A41468
60K heat shock protein htpB - Legionella pneumophila
C;Species: Legionella pneumophila
C;Species: Legionella pneumophila
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 15-Oct-1999
C;Accession: A41468; A41472
C;Accession: A41468; A41472
Ex;Hoffman, P.S; Houston, L.; Butler, C.A.
Ex;Hoffman, P.S; J330-3387, 1990
A;Title: Legionella pneumophila htpAB heat shock operon: nucleotide sequence and express A;Reference number: A41468; MUD:90382960; PMID:2205580
A;Reference number: A41468
A;Residues: 1-550 <AOF>
A;Cross-references: GB M31918
A;Cross-references: GB M31918
A;Cross-references: GB M31918
A;Cross-references: GB M31918
                                                                                                                                                                                                                                                                                                                                                                                                             R; Sampson, J.S.; O'Connor, S.P.; Holloway, B.P.; Plikaytis, B.B.; Carlone, G.M.; Mayer, Infect. Immun. 58, 3154-3157, 1990
A; Title: Nucleotide sequence of htpB, the Legionella pneumophila gene encoding the 58-ki A; Reference number: A41472; MUID: 90354095; PMID: 2117582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: DNA
A,Residues: 3-188,'S',190-195,'LIAVH',202-347,'T',349-550 <SAM>
A,Cross-references: GB:M91673; GB:M35149; NID:g149689; PIDN:AAA25298.1; PID:g149690
C;Genetics:
A;Gene: htpB
C;Superfamily: chaperonin groEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 SGRPILIIAEDVEGEALATLVVNNNRGIVKVCAVKAPGFGDRRKAMLQDIAILTKGQVIS 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 AVLAVTKKLQAMSKPCKDSKAIAQVGTISANSDEAIGAIIAEAMEKVGKEGVIIVEDGNG 183
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                                                                                                       539 DMGGMGMM 546
                                                                  540 GMGGMDGM 547
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C,Accession: 140331
R;Fernandez, R.C.; Weiss, A.A.
Gene 158, 151-152, 1995
A;Title: Cloning and sequencing of the Bordetella pertussis cpn10/cpn60 (groESL) homolog A;Reference number: 140330; MUID:95309719; PMID:7789805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 AKVNRPLLIIAEDVEGEALATLVVNKLRGALQVVAVKAPGFGERRKAMLEDIAILTGGEA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09
                     Species: Bordetella pertussis
| Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGLETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQV
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                                                                                                                                                                                                                                            Cross-references: EMBL:U12277; NID:g968918; PIDN:AAA74967.1; PID:g968920
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                                                                                                                                                                                                                                                                                                                                                                                        98; Indels
                                                                                                                                                                                                                                                                                                                                               68.1%; Score 1843.5; DB 57.4%; Pred. No. 2.7e-82; tive 74; Mismatches 98
                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
protein (GroEL) - Bordetella pertussis
                                                                                                                                                                                                                                                                                                       Superfamily: chaperonin groEL
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A;Cross_references: EMBL:0;Genetics: A;Gene: cpn60
C;Superfamily: chaperonin
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360 360 420

241 AKSGRPLLVIAEDIEGEALATLVVNNIRGVVKVAAVKAPGFGDRRKAMLODIAVLTGGKV 300

301 IFEDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDY 301 ISEEVGLSLEAASLDDLGSAKRVVVTKDDTTIIDGSGDAGDIKNRVEQIRKEIENSSSDY

241 AKVNRPLLIIAEDVEGEALATLVVNKLRGALQVVAVKAPGFGERRKAMLEDIAILTGGEA

181 SGLENALEVVEGMQFDRGYLSPYFINNQQNMSAELENPFILLVDKKISNIRELIPLLENV

181 KGLETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQV

DREKLOERLAKLVGGVAVIHVGAATETEMKEKKDRVEDALNATRAAVEEGIVPGGGTAFV

361

421 421 480

RSIKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKD-GFGFN 479

RVLKSLDSVEVENEDQRVGVEIARRAMAYPLSQIVKNTGVQAAVVADKVLNHKDVNYGYN AASGEYEDLIKAGVIDPKKVTRIALQNAASVASLLLTTECAIAEKPEPKKDMPMPGGG-M

481 AATGEYGDMIEMGILDPTKVTRTALQNAASIAGLMITTECMVTEAPK-KKEESMPGGGDM 539

540 GGMGGMGGM 548 GGMGGMDGM

539

480

240

180

120

9 09

Gaps

3

Length 552;

68.1%; Score 1843.5; DB 2; Length 66.5%; Pred. No. 2.7e-82; ive 82; Mismatches 99; Indels

Query Match Best Local Similarity 66.5% Matches 365; Conservative

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1 MASKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEI 1 MAAKVLKFSHEVLHAMSRGVEVLANAVKVTLGPKGRNVVLDKSFGAPTITKDGVSVAKEI ELEDKFENMGAQMVKEVAPKTSD1AGDGTTTATVLAQA1YREGVKLVAAGRNPMA1KRG1

A, Accession: S39765
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-552 < VOD>
A, Cross-references: GB: M20482; NID:g144996; PIDN: AAA23309.1; PID:g144998
C, Superfamily: chaperonin grobL

DKAVVAVTKELSDITKPTRDQKEIAQVGTISANSDTTIGNIIAEAMAKVGKGGVITVEEA

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61 ELEDKFENMGAQMVKEVASRTSDDAGDGTTTATVLAQAILVEGIKAVIAGMNPMDLKRGI 120

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R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernand Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A/Fille: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endos A/Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                             magar
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A;Cross-references: GB:AL591985; PIDN:CAC49406.1; PID:g15140892; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Dela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Science 293, 668-672, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
                                                                           probable heat shock protein groEL [imported] - Sinorhizobium meliloti (strain 1021)
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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RESULT 10
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C;Species: Coxiella burnetii C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 28-May-1999 C;Dacession: 339765 R;Vodkin, M.H.; Williams, J.C. J. Bacteriol. 170, 1227-1234, 1988 A;Title: A heat shock operon in Coxiella burnetii produces a major antigen homologous A;Reference number: S39764; MUID:88139182; PMID:3343219

chaperonin 60 - Coxiella burnetii

source: strain C58 (Dupont)

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A,Gene: groEL
A,Map position: circular chromosome
C,Superfamily: chaperonin groEL
             A; Experimental
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                                C, Genetics:
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GO KDA chaperonin [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AD2660
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Accession: AD2660
A;Accession: AD2660
A;Accession: AD2660
A;Accession: Genome of Che Natural Genetic Diplication of Conductive C58.
A;Molecule type: DNA
A;Residues: 1-544 cKUR>
A;Cross-references: GB:AE008688; PIDN:AAL41698.1; PID:g17739044; GSPDB:GN00186
             Ä,
               Yeh,
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hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, A, Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A; Reference number: A96039; MUID:21368234; PMID:11474104
A; Contents: annotation
C; Genetics: A; GMD21566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 AQTNEYGDLYAMGVIDPAKVVRTALQDAASVAGLLVTTEAMIAEKPKKEAAPALPAG---
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                                                                                                                                                                               68.0%; Score 1841; DB 2; Length 542;
68.3%; Pred. No. 3.5e-82;
iive 71; Mismatches 96; Indels
                                                                                                                            A, Genome: plasmid
C, Superfamily: chaperonin groEL
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60K chaperonin (protein cpn60) (groEL protein) [imported] - Agrobacterium tumefaciens (s
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C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: B97442
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 232-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
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A; Cross-references: GB: AE007869; PIDN: AAK86491.1; PID: 915155641; GSPDB: GN00169
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; Score 1840.5; DB
; Pred. No. 3.7e-82;
69; Mismatches 95
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     68.0%;
69.2%;
  Query Match
Best Local Similarity 69.2%
Matches 376; Conservative
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A; Status: preliminary
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A,Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc
A,Reference number: A82950; MUD:20437337; PMID:10984043
A,Accession: B83098
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K.; Lim,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P.; Hickey,
A.; Larbig,
             DKAVVAVTKELSDITKPTRDQKEIAQVGTISANSDTTIGNIIAEAMAKVGKGGVITVEEA 180
                                   241 AKVNRPILLIAEDVEGEALATLVVNKIRGALQVVAVKAPGFGERRKAMLEDIAILTGGEA 300
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83098
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hick adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larb ... i Lory, S.; Olson, M.V.
                                                                             KGLETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQV
                                                                                                                                                                                                           IFEDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDY
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66.8%; Pred. No. 2e-81;
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Best Local Similarity
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A; Residues: 1-547 <STO>
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R;Segal, G.; Ron, E.Z.
Submitted to the EMBL Data Library, August 1992
A;Description: Cloning and sequencing of the GroE operon of Agrobacterium tumefaciens
A;Reference number: S23917
A;Accession: S23918
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                                                                                                                                                                                                                                                                  groEL protein - Agrobacterium tumefaciens
C.Species: Agrobacterium tumefaciens
C.Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
                                                  1 MASKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEI
                                                                                                                 ELEDKFENMGAQMVKEVAPKTSDIAGDGTTTATVLAQAIYREGVKLVAAGRNPMAIKRGI
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;Cross-references: BMBL:X68263; NID:g1019913; PIDN:CAA48331.1; PID:g39095
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|MAAKEVKFGASAREKMLKGVDILADAVKVTLGFKGRNVVIDKSFGAPPITKDGVSVAKEI
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                         Indels
   Pred. No. 3.7e-82;
9: Mismatches 95;
69.2%; Pred. Active 69; Mismatches
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C;Superfamily: chaperonin groEL
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Best Local Similarity 68.9%
Matches 374; Conservative
                Matches 376; Conservative
   Best Local Similarity
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                                 AKVNRPLLIIAEDVEGEALATLVVNKLRGALQVVAVKAPGFGFRRKAMLEDIAILTGGEA 300
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Ryfor, D.; Mayfield, J.E.

Biochim. Biophys. Acta 1130, 120-122, 1992

A;Title: Cloning and nucleotide sequence of the Brucella abortus grob operon.

A;Reference number: $22346; MUID:92182006; PMID:1347461

A;Accession: $22346; MUID:92182006; PMID:1347461

A;Actus: preliminary

A;Molecule type: DNA

A;Residues: L-546 <GGR>

A;Cross-references: EMBL: M82975; NID:g144109; PIDN:AAA22997.1; PID:g144111

C;Superfamily: chaperonin grobL
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Best Local Similarity 68.9%
Matches 378; Conservative
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C;Date: 22-Nov-1993 #sequen
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us-09-077-574a-2.rsp

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

January 28, 2004, 13:10:35 ; Search time 17 Seconds (without alignments) 1515.920 Million cell updates/sec Run on:

Title: Perfect score:

US-09-077-574A-2 2708 1 MASKEILFDAKAREKLSRGV......KDMPWPGGGMGGMGGMT 548 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

127863 seqs, 47026705 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	CH60 RALSO	CH60 ACEAC	CH60 BURCE	CH60 BURPS	CH60 BURVI	CH60 RHOPA	CH60 BURTH	CH60 BARHE	CH61 RHIME	CH60 AMOPS	CH60 BARQU	CH64 RHIME	CH60_XYLFA	CH60 RHOMR	CH60 CHRVI	CH60 XANAC	CH60 RHOCA	CH60 RHILV	CH60 XANCH	CH60_BORPE	CH60_COXBU	CH60 XANCP	CH65 RHIME	CH60 AGRTS			CH62 RHILE	CH61_BRAJA	CH60 PARDE	1	1		
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1 CH60 BRUSU CH62 BRAJA 1 CH62 RHIME 1 CH60 NEIMA 1 CH60 BRUME 1 CH64 RHILO 1 CH63 RHILO	1 CH60 NEIMB 1 CH60 BARBA 1 CH60 ALTHA 1 CH65 RHILO 1 CH60 NEIGO
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ALIGNMENTS	CHEOLT 1 CHEO_RALSO D CHEO RALSO STANDARD; PRT; 547 AA.	28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) 60 kDa chaperonin (Protein Conf.) (GroR. nrotein)	MOPA OR RSC0642 (arrum (Pseudomonal cteria; Betaprotal Ralstonia.	(1) SEQUENCE FROM N.A. STRAIN-GMI1000; MEDLINE=21681879; PubMed=11823852;	Salahoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siquier P., Thebault P., Whalen M. Wincher P.	Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415.497-502 (2002)		-:- SUBGAIL: Oligomer of 14 subunits composed of two stacked rings of 7 subunits (By similarity)!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)!- SIMILARITY: Belongs to the chaperonin (HSP60) family.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)	EMBL; ALG46060; CAD14172.1; - HAMAP; MF 00600, -; 1. InterPro; IPR00184; Chaprnin Cpn60. InterPro; IPR00184; Chaprnin Cpn60. Ffam; PF00118; cpn60 TCP1, 1. PRIMTS; PR00298; CHAPERONIN60. PRIMTS; PR00304; TCOMPLEXTON. PROSITE; PS00209; CHAPERONINS CPN60; 1. Chaperone; ATP-binding; Complete proteome. SEQUENCE 547 AA; 57404 MW; 0487E4650867C25A CRC64;	Query Match Best Local Similarity 69.5%; Pred. No. 2.1e-83; Matches 380; Conservative 70; Mismatches 96; Indels 1; Gaps 1;
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SEQUENCE FROM N.A.
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Zysk G., Splettstoesser W.D., Neubauer H.;
              entities requires a license agreement (S or send an email to license@isb-sib.ch).
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last amoutation update)
60 Maa chaperonin (Protein Cpn60) (großL protein)
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
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                                                                                                                                                                                                                      Length 546;
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                                                                                                          HAMAP; MF_00600; -; 1.

Pfam; PF00118; cpn60_TCP1; 1.

PROSITE; PS00296; CHĀPERONINS_CPN60; 1.

Chaperone; ATP-binding.

SEQUENCE 546 AA; 58106 MW; 3B476AF42F2CD5CC CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
60 kDa chaperonin (Protein Cpn60) (groEL protein).
                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                    Score 1880; DB 1;
Pred. No. 7.2e-83;
9; Mismatches 94
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-!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of 7 subunits (By similarity).
-!- SUBCRIFULAR LOCATION: Cytoplasmic (By similarity).
-!- SUBCRIFULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 KGLETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
   "Nucleotide sequence comparison of the groE operon of Burkholderia
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68.4%; Pred. No. 1.6e-82;
                                                         Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
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Chaperone; ATP-binding.
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InterPro; IPR001844; Chaprnin Cpn60.
InterPro; IPR002423; Cpn60/TCP-1.
Pfam; PF00118; cpn60 TCP1; 1.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 DKAVAAVEELKKISKPCTTNKEIAQVGAISANSDSSIGDRIAEAMDKVGKEGVITVEDG 180
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                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ELEDKFENMGAQMVKEVAPKTSDIAGDGTTTATVLAQAIYREGVKLVAAGRNPMAIKRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 KGLETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQV
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                                                                                                                                                                                                                                                      Woo P.C.Y., Leung P.K.L.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Prevents misfolding and promotes the refolding and
proper assembly of unfolded polypeptides generated under stre
                                                                                                                                                                           Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 546;
                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to the chaperonin (HSP60) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.0%; Score 1868.5; DB 1; Length
68.2%; Pred. No. 2.5e-82;
:1ve 75; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  546 AA; 57145 MW; E9E9366EE8BD6ABD CRC64;
                                                                                                                                                     Burkholderia pseudomallei (Pseudomonas pseudomallei)
                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
60 kDa chaperonin (Protein Cpn60) (groEL protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAMAP, MF 00600; -; 1.
InterPro; IPR001844; Chaprnin Cpn60.
InterPro; IPR001844; Chaprnin Cpn60.
Pfam; PF00118; cpn60 TCP1; 1.
PRINTS; PR00288; CHAPERONIN60.
PROSITE; PS00304; TCOMPLEXTCP1.
Chaperone; ATP-binding.
                                    PRT;
                                                                                                                                                                                                                                                                                                                                                             subunits (By similarity).
                                                                                                                                                                     Bacteria, Proteobacteria, Betar
Burkholderiaceae, Burkholderia.
                                                                                                                                                                                                                                                                                                                             conditions (By similarity)
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                                    STANDARD:
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                                                                                                                                     GROL OR GROEL OR MOPA
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                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                         NCBI_TaxID=28450;
                                  BURPS
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RESULT 4
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                                                                                                                                                                           ASGEYEDLIKAGVIDPKKVTRIALQNAASVASLLLTTECAIAEKPERKKDMPMFGGGMGG 540
                   360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conditions (By similarity).
SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of 7 subunits (By similarity).
                                                                                                                                                                                               DREKLQERLAKLVGGVAVIHVGAATETEMKEKKDRVEDALNATRAAVEEGIVPGGGTAFV
                                                                                                             RSIKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNA
                                                                                                                                     DRBKLÓERVAKLAGGVAVIKVGAATEVEMKEKKARVEDALHÁTRAAVEBGIVPGGGVALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zysk G., Splettstoesser W.D., Neubauer H.; "Nucleotide sequence comparison of the groE operon of Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
NCBI_TaxID=60552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
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Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
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Chaperone; ATP-binding.
SEQUENCE 546 AA; 57010 MW; 47FAB93959221218 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
60 kDa chaperonin (Protein Cpn60) (groEL protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.0%; Score 1868.5; DB:
68.2%; Pred. No. 2.5e-82;
iive 75; Mismatches 96,
                                                                                                                                                                                                                                                                                                                                                             546 AA.
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InterPro; IPR001844; Chaprnin Cpn60.

InterPro; IPR00423; Cpn60/TCP-1.

Pfam; PF00118; cpn60 TCP1; 1.

PRINTS; PR00298; CHAPERCONIN60.

PRINTS; PR00304; TCOMPLEXTCP1.
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-1- SUBDNIT: Oligomer of 14 subunits composed of two stacked rings of 7 subunits (By similarity).
                                                                                                                                                                                      KGLBTTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQV
                                                                                                                                                                                                         RSIKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNA
ELKDKLÇNMGAQMVKEVASKTSDNAGDGTTTATVLAQSIVREGMKYVASGMNPMDLKRGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               palustris.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Prevents misfolding and promotes the refolding
proper assembly of unfolded polypeptides generated under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
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-!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
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60 kDa chaperonin (Protein Cpn60) (groEL protein)
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Burkholderia thailandensis.
Bacteria, Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
                                                                                                                              Length 546;
                                                                                                                                              95; Indels
                                                                                                       546 AA; 57937 MW; 163C7115D68FFFF8 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
60 kDa chaperonin (Protein Cpn60) (groEL protein).
                                                                                                                         69.0%; Score 1868; DB 1; 68.2%; Pred. No. 2.7e-82;
                                                                                                                                  68.2%; Pred. No. 2.7e
 send an email to license@isb-sib.ch)
                                                                                   PROSITE; PS00296; CHAPERONINS_CPN60; 1.
Chaperone; ATP-binding.
SEQUENCE 546 AA; 57937 MW: 163C7115
                           HAMAP; MF_00600; -; 1.
InterPro; IPR001844; Chaprnin Cpn60.
InterPro; IPR00243; Cpn60/TCP-1.
Pfam; PF00118; Cpn60 TCP1; 1.
PRINTS; PR00298; CHAPERONINGO.
PRINTS; PR00304; TCOMPLEXTCP1.
                  EMBL; AF406639; AAK94943.1; -.
                                                                                                                                         Matches 374; Conservative
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-!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
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                         'Burkholderia thailandensis chaperonin GroEL gene, complete
                                                                                                                                                                                                            7 subunits (By similarity).
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: Belongs to the chaperonin (HSP60) family.
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68.2%; Pred. No. 2.8e-82;
ive 75; Mismatches 95; Indels
                                                     sequence.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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PRINTS; PR00304; TCOMPLEXTCPI.
PROSITE; PS00296; CHAPERONINS_CPN60; 1.
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InterPro; PR001844; Chaprnin Cpn60.
InterPro; IPR002423; Cpn60/ICF-1.
Pfam. PF00118; cpn60_TCP1; 1.
Moo P.C.Y., Woo G.K.S., Yuen K.Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of 7 subunits (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
60 kDa chaperonin (Protein Cpn60) (groEL protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marston E.L., Sumner J.W., Regnery R.L.; "Evaluation of intraspecies genetic variation within the 60 kDa heat shock protein (groEL) gene of Bartonella species: a new phylogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE 1973/3904; PubMed=9230387; Summer J.W., Nicholson W.L., Massung R.F.; Summer J.W., Nicholson W.L., Massung R.F.; Summer J.W., Nicholson W.L., Massung R.F.; Summer J.W., Nicholson W.L., Massung proess."; J. Clin. Microbiol. 35:2087-2092(1997).

-!- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions (By similarity).
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=ATCC 49882 / Houston 1;
STRAIN=ATCC 49889; PubMed=9274034;
Haake D.A., Summers T.A., MCCOy A.M., Schwartzman W.;
Heak shock response and groEL sequence of Bartonella henselae and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.0%; Score 1867.5; DB 1; Length 547; 70.1%; Pred. No. 2.8e-82;
                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bartonellaceae; Bartonella.
NCBI_TaxID=38323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases
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                                                                                        547 AA
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InterPro; IPR001844; Chaprnin Cpn60.
InterPro; IPR001844; Cpn60/TCP-1.
InterPro; IPR002423; Cpn60/TCP-1.
Pfan; PP00118; cpn60 TCP1; 1.
PRINTS; PR00298; CHAPEROXIN60.
PRINTS; PR00304; TCOMPLEXTCP1.
PROSITE; PS00304; TCAMPLEXTCP1.
Chaperone; ATP-binding; Pleat Bonck.
                                                                                                                                                                                                                  Bartonella henselae (Rochalimaea henselae)
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                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE OF 1-408 FROM N.A.
STRAIN=ATCC 49882 / Houston 1;
MEDLINE=97373904; PubMed=9230387;
                                                                                                                                                                                                                                                                                                                                                                                              Microbiology 143:2807-2815(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ATCC 49882 / Houston 1;
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HSSP; P06139; 1GRL.
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                                                                                          STANDARD;
                                                                                                                                                                                                          GROEL OR MOPA
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             539 MGGM-GM 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              analysis tool."
                                                                                           CH60 BARHE
033963; 087267;
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Best Local
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                                                                              CH60 BARHE
                                                            RESULT 8
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Local Similarity

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301 IFEDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDY 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 RSIKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPK-DGFGFN 479
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                                                                                                                                                                                                                                                                                         241 VQSGKPLLIIAEDVEGEALATLVVNKLRGGLKIAAVKAPGFGDRRKAMLEDIAILTSGQV 300
                                                                   120
                                                                                                                                                                  121 DAAVDEVVANLFKKAKKIQTSAEIAQVGTISANGAAEIGKMIADAMEKVGNEGVITVEEA 180
                                                                                                                                                                                                    KGLETTLDVVEGMKEDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQV 240
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                                                                                                                                    DKAVVAVTKELSDITKPTRDQKEIAQVGTISANSDTTIGNIIAEAMAKVGKGGVITVEEA
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1 MASKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 39, Last sequence update)
28-FEB-2000 (Rel. 41, Last annotation update)
60 kDa chaperonin 1 (Protein Cpn60 1) (groEL protein 1).
60 kDa chaperonin 1 (Protein Cpn60 1) (groEL protein 1).
61 kDa chaperonin 1 (Sinorhizobium meliloti (Sinorhizobium meliloti (Sinorhizobium meliloti).
8 Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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MEDLINE=93231539; PubMed=8097179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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6; Gaps
                                                                                                                                                                                                                                                                                             conditions (By similarity).
-1- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings 7 subunits (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                              -! SIMILARITY: Belongs to the chaperonin (HSP60) family.
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Pred. No. 3e-82;
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InterPro; IPR001844; Chaptnin Cpn60.

InterPro; IPR002423; Cpn60/TCP-1.

Pfam; PF00118; cpn60 TCP1; 1.

PRINTS; PR00399; CHAPERONINS.

PROSITE; PS00296; CHAPERONINS_CPN60; 1.

Chaperone; ATP-binding; Heat shock; Multigene family;
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; 4CEF358957E1B45A CRC64;
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PIR, VANDSO9, JNDSO9.
HSSP, PO6139; IGRL.
HAMAP, MF_00600; ...
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between the swiss institute. There are no restrictions the European Bioinformatics Institute. There are no restrictions as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Www.isb-sib.ch/announce/
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R-SIKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPK-DGFGF 478
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                     479 NAASGEYEDLIKAGVIDPKKVTRIALQNAASVASLLLTTECAIAEKPEPKKDMPMPGGGM
                                                                                                          479 NAQTGEYGDMIAMGIIDPVKVVRTALQDAASVASLLITTEAMIAEL--PKKDAPAMPGGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conditions (By similarity).
-!- SUBDUIT: Oligomer of 14 subunits composed of two stacked rings of 7 subunits (By similarity).
-!- SUBCELLULAR LOCATION: Oytoplasmic (By similarity).
-!- SUBCELLULAR LOCATION: Oytoplasmic (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ahn T.I., Leotide sequence and temperature-dependent expression of groEL gene isolated from symbiotic bacteria of Amoeba proteus.", Endocyt. Cell Res. 8:33-44(1991).
-!- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress.
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                                                                                                                                                                                                                                                                                                                                                                                                              Amoeba proteus symbiotic bacterium.
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
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                                                                                                                                                                                                                                                                                                                  01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
60 kDa_chaperonin (Protein Cpn60) (groEL protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.9%; Score 1866; DB 1; 67.9%; Pred. No. 3.4e-82;
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PRINTS; PRO0304; TCOMPLEXTCP1.
PROSITE; PS00296; CHAPERONINS_CPN60; 1.
Chaperone; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF 00600; -; 1.
InterPro; IPR001844; Chaprnin Cpn60.
InterPro; IPR002423; Cpn60/TCP-1.
Pfam; PF00118; cpn60_TCP1; 1.
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PIR; JC2562; JC2562.
HSSP; P06139; 1GRL.
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                                                                                                                                                   539 GGMGGMDGM 547
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HSSP; P06139; 1GRL.
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                                                                                                                            VNRPLLIIAEDVEGEALATLVVNKLRGALQVVAVKAPGFGERRKAMLEDIAILTGGEAIF 302
                                                                                                                                             Bartonella quintana.";
Microbiology 143:2807-2815(1997).
-!- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions (By similarity).
-!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
60 kDa chaperonin (Protein Cpn60) (groEL protein) (Heat shock protein
                 AVVAVTKELSDITKPTRDQKEIAQVGTISANSDTTIGNIIAEAMAKVGKGGVITVEBAKG
                                      AVTAITKELQKWSKPCKDGKAIAQVGTISANSDQAIGSIIAEAMEKVGKEGVITVEDGNG
                                                                     LETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQVAK
                                                                                     423 IKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNAAS
                                                                                                                                                                                  EDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDYDR
                                                                                                                                                                                                                                       EKLOERLAKIVGGVAVIHVGAATETEMKEKKDRVEDALNATRAAVEEGIVPGGGTAFVRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97419519; PubMed=9274034; Haake D.A., Subwartzman W.; Haake D.A., Summers T.A., MCCoy A.M., Schwartzman W.; "Heat shock response and groEL sequence of Bartonella henselae and
                                                                                                                                                                                                                                                                                                                                                  GEYEDLIKAGVIDPKKVTRIALQNAASVASLLLTTECAIAEKPEPKKDMPMPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bartonella quintana (Rochalimaea quintana).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bartonellaceae; Bartonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to the chaperonin (HSP60) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      547 AA
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EMBL; U78515; AAB69095.1; -.

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                                                                                                                                                                                    DB 1; Length 547;
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                                                                                                                                                                                  ; Score 1864.5; DB 1; Length
; Pred. No. 4e-82;
61; Mismatches 96; Indels
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
60 kDa chaperonin 4 (Protein Cpn60 4) (groEL)
6ROL4 OR GROEL4 OR RA0335 OR SWA0744.

Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymA (megaplasmid 1)
HAMAR; MF 00600; -; 1.
InterPro; IPR001844; Chaprnin Cpn60.
InterPro; IPR001844; Cpn60/TCF-1.
Pfan; PF00118; cpn60 TCF1; 1.
PRINTS; PR00298; CHAPERONIN60.
PRINTS; PR00304; TCOMPLEXTCP1.
PROSITE; PS00296; CHAPERONINS_CPN60; 1.
Chaperone; ATP-binding; Heat Shock.
SEQUENCE 547 AA; 57610 MW; 8620CFC50BF
                                                                                                                                                                                      68.98;
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PIR; F82783; F82783.
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28-FEB-2003 (;
28-FEB-2003 (;
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CH60_XYLFA
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             Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.,
"Nucleotide sequence and predicted functions of the entire
                                                                                                                                                                                                                                        conditions (By similarity).
-1- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of 7 subunits (By similarity).
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                                                                                                                                                Sinorhizobium meliloti pSymA megaplasmid.",
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
-!- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress
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Chaperone; ATP-binding; Heat shock; Multigene family; Plasmid;
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                                                                                                                                                                                                                                                                                                                                                                                                  the Swiss Institute of Bioinformatics and the
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                                                                                                                                                                                                                                                                                                                                                                                                                  the Buropean Bioinformatics Institute. They use by non-profit institutions as long amodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; C95311; C95311.

HAMAP; MF_00600; -; 1.

InterPro; IPR001844; Chaprnin Cpn60.

InterPro; IPR002423; Cpn60/TCP-1.

Pfan; PF00118; Cpn60 TCP1; 1.

PRINTS; PR00298; CHAPERONINGO.

PRINTS; PR00304; TCOMPLEXTCP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         requires a license agreement
MEDLINE=21396509; PubMed=11481432;
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SEQUENCE 545 AA;
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SOW WWW WAR BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK BRANK 
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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NAASGEYEDLIKAGVIDPKKVTRIALQNAASVASLLLTTECAIAEKPEPKKDMPMPGGGM 538
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A Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
A Alvarenga R., Alves Lu.M.C., Arruda P., Baha G.S., Baptista C.S.,
A Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
Bueno M.R.P., Camargo A.A., Camargo L.E., Cartarro D.M., Carter H.,
Bueno M.R.P., Caladro A.A., Canararo D.M., Carter H.,
Colauto N.B., Colombo C., Costa P.F., Costa M.C.R., Costa-Noto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
Ra Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
Radricani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
Radarnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
A Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Kitajima J.P.,
Rrieger J.S., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
A Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
A Marchado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
A Manchado M.A., Materias E.C., Maylaxi C.Y., Monteiro-Vitorello C.B.,
A Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
A Nandai M.J., Nobrega F.C., Palmieri D.A., Perguero J.B.,
A Peixoto B.R., Pereira G.A.G., Rodrigues V., de Rosa A.J.M.,
A de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
A da Silvaira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
A de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
A da Silvaira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.B.,
A dalada H., Van Sluys M.A., Truffi D., Truffi D., Truffi D., Truffi D., Truffi D., Truffi D., Truffi D., Truffi D., Truffi D., Truffi D., Truffi D., Truffi D., Truffi D., Truffi D., Truffi D., Truffi D., Truffi D., Truffi D., Truffi D., Truffi D., Truffi D., Sayana D., Truffi D., Sayana D., Truffi D., Sayana D., Truffi D., Sayana D., Sayana D., Sayana D., Sayana D., Sayana D., Sayana D., Sayana D., Sayana D., Sayana D., Sayana D., Sayana D., Sayana D., Sayana D., Sayana D., Sayana D., Sayana D., Sayana D., Sayana D., Sayana D., Sayana D., Sayana D., Sayana 
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-!- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
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Xanthomonadaceae; Xylella.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
60 kDa chaperonin (Protein Cpn60) (grobL protein)
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MEDLINE=20365717; PubMed=10910347;
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Xylella fastidiosa.
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Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;
Crenotrichaceae; Rhodothermus.
                                                                                                               DB 1; Length
                                                                                                                                 97; Indels
           HAMAP; MF_00600; -; 1.

InterPro; IPR001844; Chaprnin Cpn60.

InterPro; IPR00243; Cpn60/TCP-1.

Pfam; PF00118; cpn60 TCP1, 1.

PRINTS; PR00298; CHAPERONIN60.

PRINTS; PR00304; TCOMPLEXTCP1.

PROSITE; PS00296; CHAPERONINS_CPN60; 1.

Chaperone; Aff-binding; Complete proteome.

SEQUENCE 547 AA; 57757 MW; 30BE7F937CA7A9D8 CRC64;
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STRAIN=ITI 376;
Thorolfsdottir E.T.T., Backman V.M., Blondal T.,
                                                                                                              68.8%; Score 1862.5; DB
ilarity 66.8%; Pred. No. 4.9e-82;
Conservative 80; Mismatches 97
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                   Kristjansdottir S., Eggertsson G.; "Heat shock in Rhodothermus marinus: cloning and sequence analysis the großEL, dnaK and dnaJ genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASGEYEDLIKAGVIDPKKVTRIALQNAASVASLLLTTECAIAEKPEPKK-DMPMPG
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                                                                                                                                                                                        conditions (By similarity). SUBUNIT: Oligomer of 14 subunits composed of two stacked
                                                                                                                             -!- FUNCTION: prevents misfolding and promotes the refolding proper assembly of unfolded polypeptides generated under
                                                                                                                                                                                                                                          7 subunits (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the chaperonin (HSP60) family.
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93; Indels
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Chaperone; ATP-binding.
SEQUENCE 540 AA; 57666 MW; 6867448B7BEF18EC CRC64;
Thorbjarnardottir S.H., Palsdottir A., Hauksdottir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.4%; Score 1004.0.
69.2%; Pred. No. 1.5e-81
tive 71; Mismatches !
                                                                                                    Submitted (APR-1999) to the EMBL/GenBank/DDBJ
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InterPro; IPR001844; Chaprnin Cpn60.
InterPro; IPR00243; Cpn60/TCP-1.
Pfam, PF00118; Cpn60 TCP1; 1.
PRINTS; PR00298; CHAPERONINGO.
PRINTS; PR00304; TCOMPLEXTCP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF145252; AAD37976.1; -.
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les 371; Conservative
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J, characterization, and functional expression in Escherichia

chaperonin (grobSL) genes from the phototrophic sulfur
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-!- FUNCTION: Prevents misfolding and promotes the refolding and
Proper assembly of unfolded polypeptides generated under stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                Diomisi H.M., Viale A.M.;
Purification and characterization of Chromatium vinosum GroEL and
GroES proteins overexpressed in Escherichia coli cells lacking the
endogenous groESL operon.";
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                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
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Chaperone; ATP-binding.
SEQUENCE 546 AA; 57541 MW; 3250141881C04DD6 CRC64;
                                                                     01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
60 kDa chaperonin (Protein Cpn60) (groEL protein).
GROL OR GROEL OR MOPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.4%; Score 1852.5; DB : 68.2%; Pred. No. 1.5e-81;
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InterPro; IPR001844; Chaprnin_Cpn60.
InterPro; IPR00243; Cpn60/TCP-1.
Pfam: PF00118; cpn60_TCP1; 1.
PRINTS; PR00298; CHAPERSONINGO.
PRINTS; PR00304; TCOMPLEXTCP1.
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CHARACTERIZATION.
MEDLINE=99008942; PubMed=9790891;
                                                                                                                                                                                                                                                                                                                                                      bacterium Chromatium_vinosum.";
J. Bacteriol. 175:1514-1523(1993).
                                                                                                                                                                                                                                                                             MEDLINE=93186721; Pubmed=8444812;
Ferreyra R., Soncini F., Viale A.!
"Cloning, characterization, and f
                                                                                                                                                                                                      Chromatiaceae, Allochromatium.
NCBI_TaxID=1049;
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Best Local Similarity
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                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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CH60_CHRVI
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O31198 ]
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                       OM protein - protein search, using sw model
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OBCENT OFFICE TESTS THE TE	OBCWJO	16	532	60.7	1644	45
Ogrio finesotori	086700	7	539	6.09	1648.5	44
	08GBB8	~	532	61.3	1659	43
1 00	Q8GBC8	N	532	61.3	1660	42
	087271	7	503	61.3	1660	41
OBKINS STREETOCOCCII	Q8KJ08	7	535	61.4	1663	40
	QBGBC2	N	531	61.4	1663	39
	Q9X4R5	7	540	61.4	1663.5	38
	Q8KJ12	~	534	61.6	n	3.7
08kiv3 streptococo	Q8KIY3	N	534	9.19	1668	36
-	QAGBCO	7	531	61.6	1669	35
ORabot enterococcu	O8GBC4	Ċ	531	61.6	1669	34
	OBGBC6	~	531	61.7	1670	33
ONGENO SET SELECTION	008200	~	548	61.7	1671.5	32
Vegbbe streptococc	008499	N	548		1672.5	31
	OBCBBC	0	534	61.9	1675	30
pucimera	OBKTWO	c	537	61.9	1676.5	29
	OSKTW3	1 (1	537	62.0	1679.5	28
	O8K.T10	۱۸	53.6	62.1	1681	27
Section Services	ORKTW4	~	537	62.2	1683.5	26
ے س	08CX00	16	540	62.2	1685	25
Obobdo antimococc	OBGBDO	7	531	62.2	1685	24
	08CX22	16	540	62.3	1686	23
מ	O8CX1.3	16	545	62.3	1687	
Coris Duciniera Sp	O8K.714	N	537	62.4	1691	21
Vecwwe Bureptococc	OSKTW2	2	536	62.5	1691.5	20
۳,	ORCWWR	16	542	62.6	1694	19
Covers covers sp	09X603	7	555	63.0	1706	
	OBKTW7	0	548	63.2	1710.5	17

ALIGNMENTS

CONDITIONS (BY SIMILARITY).
-!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
7 SUBUNIT: SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
EMBL; U45241; AAC36500.1; -HSSP; P06139; 1GRL. "Identification and sequencing of the groE operon and flanking genes of Lawsonia intracellularis: use in phylogeny.";
Microbiology 144:0-0(0)
Microbiology 144:0-0(0)
Microbiology 148:0-0(0)
Microbio SEQUENCE FROM N.A. MEDINE-99386497; PubMed=9720028; Dale C.J.H., Moses E.K., Ong C.C., Morrow C.J., Reed M.B., Hasse D., Strugnell R.A.; Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Created)
Last sequence update)
Last amotation update)
chaperonin) (Protein Cpn60) (groEL InterPro; IPR01844; Chaprnin Cpn60.
InterPro; IPR01844; Chaprnin Cpn60.
Pfam; PF00118; cpn60 TCP1; 1.
PRINTS; PR00298; CHAPERONIN60.
PRINTS; PR00304; TCOMPLEXTCP1.
PROSITE; PS00296; CHAPERONINS CPN60; 1.
PROSITE; PS00296; Plasmid.
SEQUENCE 548 AA; 58605 MW; 6388C431E663E498 CRC64; 548 AA. PRT; Desulfovibrionaceae; Lawsonia. 01-OCT-2002 (TrEMBLrel. 22, GroEL/HSP60 homolog (60 kDa Lawsonia intracellularis. PRELIMINARY; (TrEMBLrel. (TrEMBLrel. NCBI_TaxID=29546; Plasmid pISI-2 01-NOV-1998 (01-NOV-1998 (01-OCT-2002 (087888 protein) RESULT 1 087888

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"Cloning and Characterization of groEL Operon in Acetobacter aceti.";
"Llosci. Bioeng. 94:140-147(2002).
EMBL; ABO81586; BAc16232.1; -.
SEOUENCE 546 AA; 58106 MW; 3E476AF42F2CD5CC CRC64;
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Acetobacteraceae, Acetobacter.
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100.0%; Score 2708; DB 2; 100.0%; Pred. No. 1.3e-124;
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-!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
BENDL, AL672115; CAD31231.1; -- IMPROPER OF 1 PRO01844; Chaptain Cpn60.
InterPro; IPR001844; Chaptain Cpn60.
InterPro; IPR002423; Cpn60/TCP-1.
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J. Bacteriol. 184:3086-3095(2002).

PROPER ASSEMBLY OF UNFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDING AND PROMOTES THE REFOLDING AND STREAS
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Probable chaperonin groEL DF protein (60 kDa chaperonin) (Protein Chock) (groEL protein).
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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TIGR; BRA0195; -
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Paulsen I.T., Seshadri R., Nelson K.B., Eisen J.A., Heidelberg J.F.,
Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.
                                                                                                              8;
                                                                                   67.3%; Score 1823; DB 2; Length 552; 67.8%; Pred. No. 2.2e-81;
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                                              7: Chaperone.
552 AA; 57747 MW; 7D0A8C53CD7FA6AB CRC64;
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Pfam; PF00118; cpn60 TCP1; 1.
PRINTS; PR00298; CHAPERONIN60.
PRINTS; PR00304; TCOMPLEXTCP1.
PROSITE; PS00236; CHAPERONINS_CPN60; 1.
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GROEL OR BRA0195.
Brucella suis.
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Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.; The Brucella suits genome reveals fundamental similarities between animal and plant pathogens and symbionts."; Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).
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Heliobacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                          67.2%; Score 1819; DB 16; Length 68.7%; Pred. No. 3.4e-81; Live 64; Mismatches 100; Indels
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Raymond J., Zhaxybayeva O., Gogarten J.P., Gerdes S.Y.,
Blankenship R.E.;
"Whole-genome analysis of photosynthetic prokaryotes.";
                                                                                                                                                                                                                                                                                                                                            546 AA; 57501 MW; 2E4046EDC121A30A CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
00 kDa chaperonin großL (Fragment).
Heliobacillus mobilis.
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Matches 377; Conservative
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                                                                                                                                                                                   EDKFENMGAQMVKEVAPKTSDIAGDGTTTATVLAQAIYREGVKLVAAGRNPMAIKRGIDK 122
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                               Mendybaeva N., Koukharenko
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Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Pseudoalteromonas.
                                                                                                                         3;
                                                                                                      545;
                                                                                                      DB 2; Length
                      SEQUENCE FROM N.A.
Liolios K.G., Chu L., Ostrovskaya O., Mendybaeva N., Kou
Gerdes S., Kyrpides N., Overbeek R.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY142910; ANN87514.1; -.
                                                                                  57927 MW; B9F6DB02DBC18383 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
groEL protein (60 kDa chaperonin) (Protein Cpn60).
                                                                                                      66.6%; Score 1804.5; DB 65.9%; Pred. No. 1.7e-80;
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                                                                                                                           84; Mismatches
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"Moleculer chaperone of Psychrophile.";
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                                                                                               OF.
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PREVENTS MISPOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNPOLDED POLYPEPTIDES GENERATED UNDER STRESS
                                                                         CONDITIONS (BY SIMILARITY).
-:- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS
-:- SUBUNITS (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
EMBL; ABOS7417; BAB39465.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 549;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    66.3%; Score 1796.5; DB 2;
65.7%; Pred. No. 4.3e-80;
tive 79; Mismatches 108;
                                                                                                                                                                                                           InterPro; IPR001844; Chaprnin Cpn60.
InterPro; IPR002423; Cpn60/TCP-1.
Pfam; PF00118; cpn60 TCP1; 1.
PRINTS; PR00298; CAPERONINGO.
PRINTS; PR00304; TCOMPLEXTCP1.
PROSITE; PS002296; CHAPERONINS_CPN60; 1.
ATP_binding; Chaperone.
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01-MAR-2003
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                                                                                Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Elsen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daudherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Peldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                 61 ELEDKFENMGAQMVKEVAPKTSDIAGDGTTTATVLAQAIYREGVKLVAAGRNPMAIKRGI
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                                                                                                                                                                                                                                                                                65.7%; Score 1780.5; DB 16; Length 545; 65.4%; Pred. No. 2.5e-79; ative 78; Mismatches 108; Indels 3;
                                                                                                                                                                                                                                                         545 AA; 57079 MW; 7591870B017DD521 CRC64;
                                                                                                                                                                                            Shewanella oneidensis.";
Nat. Biotechnol. 20:1118-1123(2002).
EMBL; AE015516; AAN53782.1;
                                                                       MEDLINE=22297686; PubMed=12368813;
                                                                                                                                                                                                                                                                                                       Matches 358; Conservative
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                         NCBI_TaxID=70863;
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                                                 SEQUENCE
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PRT;

Q8GBB4; 01-MAR-2003 (TrEMBLrel. 23, Created)

PRELIMINARY;

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181 KGLETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILBQV 240
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                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
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                                                                                                                                                                                                                                                                                                                                                                              Ferat J.-L., Legouar M., Michel F.,
"An active group II intron has invaded the genus Azotoba.
inserted within the essential groEL gene.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AY057439; AAL25964.1; -.
SEQUENCE 546 AA; 56875 MW; 8E1F4CC93E42A619 CRC64;
(TrEMBLrel. 23, Last sequence update) (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                             MEDLINE=93323980; PubMed=7687328;
Ferat J.L., Michel F.;
"Group II self-splicing introns in bacteria.";
Nature 364:358-361(1993).
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Kondo A., Yohda M.;

Kondo A., Yohda M.;

"Cpn60/10 from Bacillus strain MS.";

"Cpn60/10 from Bacillus strain MS.";

"Cpn60/10 from Bacillus strain MS.";

"Cpn60/10 from Bacillus strain MS.";

"Cpn60/10 from Bacillus strain MS.";

"Consilius Bacillus And PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPERTIDES GENERATED UNDER STRESS

CONDITIONS (BY SIMILARITY)

"SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS; BALONGS TO THE CHAPERONIN (HSP60) FAMILY.

"SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS; PRO0139; IGRL,

"InterPro; IPRO0144; Chaptrin, Cpn60.

"RESP: Pro0139; IGRL,

"TherPro; IPRO0144; Chaptrin, Cpn60.

"TherPro; IPRO0144; Chaptrin, Cpn60.

"TherPro; IPRO0143; Cpn60/TCP-1.

"PRINTS; PRO0109; CTGAPERONINS, CPN60; 1.

"TherPro; Prod118; Chaptrin Complexity Complexity Chaptrin Complexity Chaptrin Complexity Chaptrin Complexity Chaptrin Complexity Chaptrin Complexity Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chaptrin Chapt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AKBIKFSEBARRAMLRGVDKLADAVKVILGFKGRNVVLEKKFGSPLITNDGVTIAKEIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.3%; Score 1768; DB 2; Length 539;
65.0%; Pred. No. 1e-78;
cive 85; Mismatches 98; Indels
                                                                                                                              Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=96470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           539 AA; 57346 MW; 95626C980E30C46F CRC64;
                              01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-0CT-2002 (TrEMBLrel. 22, Last annotation update) Protein Cpn60 (60 kDa chaperonin) (groEL protein).
                 01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 354; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                        Bacillus sp. MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Op
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543 GMDGM 547

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423 IKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNAAS 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 AVVAVTKELSDITKPTRDQKEIAQVGTISANSDTTIGNIIAEAMAKVGKGGVITVEEAKG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQVAK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 VNRPLLIIAEDVEGEALATLVVNKLRGALQVVAVKAPGFGERRKAMLEDIAILTGGEAIF 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 AGKPLVIISBEVEGEALATIVVNTLRKTISCVAVKAPGFGDRRKSMLEDIAILTGGQVIS 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 SKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEIEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
EMBL; AF032910; AAB86965.1; --
                                                                                                                                                                                                                                                                                                                                                   Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=HY-1;
Kim M.J., Ahn B.Y.;
submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRI PROPER ASSEMBLY OF UNFOLDED FOLYPEPTIDES GENERATED UNDER STRI CONDITIONS (BY SIMILARITY).
                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Heat shock protein 58 (60 kDa chaperonin) (Protein Cpn60) (groEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 64.4%; Pred. No. 1e-78;
Matches 352; Conservative 86; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       546 AA; 57969 MW; 15BC9EC0A8E2A6E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, P06139; IGRL.
InterPro; IPR001844; Chaprnin Cpn60.
InterPro; IPR001844; Cpn60/TCP-1.
InterPro; IPR00242; Cpn60/TCP-1.
PRINTS; PR00189; CTAPEROXIN60.
PRINTS; PR00309; TCOMPLEXTCP1.
PROSITE; PS00256; CHAPEROXINS.
AIP-binding; Chaperone.
                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                      Leptospira interrogans.
538
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=173;
534 DMGGM
                                                                                                                                                                                                                                                                                protein).
HSP58.
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423 IKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNAAS 482
                                                                                                                    483 GEYEDLIKAGVIDPKKVTRIALQNAASVASLLLITTECALAEKPEPKKDMPMPGGGMGGMG 542
          301 EELGRELKSTTIASLGRASKVVVTKENTTIVEGAGDSDRIKARINQIRAQLEETTSEFDR 360
                                       363 EKLQERLAKLVGGVAVIHVGAATETEMKEKKDRVEDALNATRAAVEEGIVPGGGTAFVRS 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ELEDKFENMGAQMVKEVAPKTSDIAGDGTTTATVLAQAIYREGVKLVAAGRNPMAIKRGI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 DKAVVAAVEELKALSVPCSDSKAlAQVGTISANSDETVGKLIAEAMDKVGKEGVITVEDG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 KGLETTLDVVEGMKFDRGYLSPYFVTNPEKMYCELDNPYILCNEKKITSMKDMLPILEQV 240
                                                                                                                                                                               SEQUENCE FROM N.A.
Yoshida N., Oeda K., Watanabe E., Mikami T., Fukita Y., Nishimura K.,
Komai K., Matsuda K.;
Washida N., Oeduced by endosymbionts in antlions as a paralytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    toxin against insects.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).
-!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 DKAVVAVTKELSDITKPTRDQKEIAQVGTISANSDTTIGNIIAEAMAKYGKGGVITVEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MASKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Enterobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.7%; Pred. No. 1.34-7.,
tive 73; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TEMBLrel. 19, Created)
01-DEC-2001 (TEMBLrel. 19, Last sequence update)
01-MEX-2003 (TEMBLrel. 23, Last amnotation update)
großL-like protein (60 kDa chaperonin) (Protein Cpn60)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.3%; Score 1742; DB 2; 64.7%; Pred. No. 1.9e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacter aerogenes (Aerobacter aerogenes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AF306521; AAL09389.1, -...
InterPro; IPR001844; Chaprnin Cpn60.
InterPro; IPR002423; Cpn60/TCP-1.
PRINTS: PR00298; CTAPERONINGO.
PRINTS; PR00309; TCOMPLEXTCP1.
PROSITE; PS00304; TCOMPLEXTCP1.
ATP-binding; Chaperone.
                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 64.74
Matches 353; Conservative
                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                      534 DMGGM 538
                                                                                                                                                                                                                          543 GMDGM 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=548;
                                                                                                                                                                                                                                                                                                                                                                                                                       protein).
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                                               QEAVGSLK-LDGDEATGAKIIFRALEEPIRMITSNAGLEGGVIVEHAKAKKGNEGFNALT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'n.
                                       --GGG 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 LETTLDVVEGMKFDRGYLSPYFVTNPEKMVCELDNPYILCNEKKITSMKDMLPILEQVAK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 VNRPILLIAEDVEGEALATLVVNKLRGALQVVAVKAPGFGERRKAMLEDIAILTGGEAIF 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIBETSSDYDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRE
                                                                                                                                                                                                                                                                                                                                                                                          Snapyan M., Gochikyan A., Weigel P., Sakanyan V.;
"Effect of thermostable chaperonins on synthesis of proteins in
                            483 GEYEDLIKAGVIDPKKVTRIALQNAASVASLLLTTECAIAEKPEPKKDMPMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.8%; Score 1754; DB 2; Length 539; 64.6%; Pred. No. 4.9e-78; ive 87; Mismatches 98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   539 AA; 57293 MW; 2F51B6FFBB887428 CRC64;
                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
groEL protein (60 kDa chaperonin) (Protein Cpn60).
                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillales; Geobacillus.
                                                                                                                                                                                                  539 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR01844; Chaprnin Cpn60.
InterPro; IPR002423; Cpn60/TCP-1.
Pram; PP00118; Cpn60 TCP1; 1.
PRINTS; PR00298; CHAPERONINGO.
PRINTS; PR00304; TCOMPLEXTCP1.
PROSITE; PS00296; CHAPERONINS_CPN60; 1.
                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                      Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity Var... Matches 352; Conservative
                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding; Chaperone.
                                                                                       538 MGGMGGM 544
                                                                                                                     539 MGGMGGM 545
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                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ATCC31783
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                                                                                                                                                                                                                                                                                                                                                                                                                            vitro.";
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                                                                                                                                                                                             Q9EZV4
                                                                                                                                                                 RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      primary endosymbiont of Sitophilus oryzae.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae.
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-!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRI
                                                                                                                                                                                                                                                                                                                                                                                                                                            groEL protein (60 kDa chaperonin) (Protein Cpn60) (Fragment)
GROEL.
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-!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STAC

7 SUBUNITS (BY SIMILARITY)

-!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY:

EMBL; AF005236; AAB97670.1; --

HSSP; P06139; 1JON
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                                                                                                                                                                                                                                                                                                                                                                                  538 AA.
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InterPro; IPR002423; Cpn60/TCP-1.
Prim; PP00118; cpn60 TCP1; 1.
PRINTS; PR00298; CHAPERONIN60.
PRINTS; PR00304; TCOMPLEXTCP1.
PROSITE; PS00296; CHAPERONINS_CPN60; 1.
ATP-binding; Chaperone.
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01-MAR-2003
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Garcia-de la Guarda R., Urra S., Venegas A.;
"Serological response to Helicobacter pylori recombinant antigens in
Chilean infected patients with duodenal ulcer, non-ulcer dyspepsia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSIKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNA
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Heat shock protein B subunit (60 kDa chaperonin) (Frotein Cpn60)
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MEDLINE=20123532; PubMed=10660136;
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APMIS 107:1069-1078(1999)
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01-JUN-2002
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5 9

Gaps

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81; Mismatches 109; Indels

Matches 348; Conservative

Sest Local Similarity

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Delmotte F.
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).
-!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
INTERPRO, 1PR001844; Chaptnin Cpn60.
InterPro, 1PR001844; Chaptnin Cpn60.
Pfam; PF00118; Cpn60/TCP-1.
                                                                                                                                                                                                                 3 SKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEIEL
                                                                                                                                                                                                                                                                          AKEIKKSDSÄRNLLFEGVRQLHDAVKVTMGPRGRNVLIQKSYGAPSITKDGVSVAKEIEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Buchnera.
NCBI_TaxID=168690;
                                                                                                                                                                         Score 1722.5; DB 2; Length 546; Pred. No. 1.7e-76;
                                                                                                                                                 546 AA; 58242 MW; B3DAE13619F26B32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) großL protein (60 kDa chaperonin) (Protein Cpn60).
                                                                                                                                                                                64.1%; Pred. No 1.7c.7c.
tive 73; Mismatches 120;
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                                                                                                                Pfam; PF00118; cpn60 TCP1; 1. PROSITE; PS00296; CHAPERONINS_CPN60; 1. ATP-binding; Chaperone.
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Matches 350; Conservative
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01-OCT-2002 (
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                                                                                                                                                                                                                                                                                               -!- SUBUNIT: OLICOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
EMBL; AJ344978; CAC86559.1; -.
SEQUENCE FROM N.A.
STRAIN=150 Neuville-1;
Delmotte F., Sabater B., Simon J.C., Latorre A.;
"Coevolution between mitochondrialand simbiotic DNA at intraspecific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MASKEILFDAKAREKLSRGVDKLANAVKVTLGPKGRNVVIEKSFGSPVITKDGVSVAKEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 IFEDRGIKLENVSLSSLGTAKRVVIDKENTTIVDGAGKSEDIKARVKQIRAQIEETSSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DREKLQERLAKLVGGVAVIHVGAATETEMKEKKDRVEDALNATRAAVEEGIYPGGGTAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 DKEKLNERLAKLSGGVAVLKVGAATEVEMKEKKARVEDALHATRAAVEEGVVAGGGVALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSIKVLDDIKPADDDELAGLNIIRRSLEEPLRQIAANAGYEGSIVVEKVREPKDGFGFNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 ASGEYEDLIKAGVIDPKKVTRIALONAASVASLLLTTECAIAEKPEPKKD---MPMPGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 548;
                                                                                                                                                                                                           Thesis (2001), University of Valencia, Spain.
-!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER
                                                                                                     Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          548 AA; 57853 MW; 659886423C19529D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1714.5; DB : Pred. No. 4.3e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.3%; Scc...
61.8%; Pred. No. 4...
ive 92; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001844; Chaprin Cpn60.
InterPro; IPR002423; Cpn60/TCP-1.
Pfam; PF00118; Cpn60 TCP1, 1.
PRINTS; PR00298; CIAPERONINGO.
PRINTS; PR00304; TCOMPLEXTCP1.
PROSITE; PS00296; CHAPERONING_CPN60; 1.
                                                                                                                                                                                                                                                                              CONDITIONS (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 61.8
Matches 338, Conservative
                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=150 Neuville-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP-binding; Chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                538 MGGMGGM 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 MGGMGGM 547
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Search completed: January 28, 2004, 13:17:17 Job time : 42 secs